

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 16:19:15 ; Search time 5274 Seconds

(without alignments)  
10706.087 Million cell updates/sec

Title: US-09-655-272-1\_COPY\_284\_1477

Perfect score: 1194

Sequence: 1 atgcgcagcaccacactct.....gagacaagcgctgcgggtg 1194

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194	100.0	1794	6 AX018705	AX018705 Sequence
2	1194	100.0	1794	6 BD140670	BD140670 Novel mam
3	1194	100.0	1795	10 AF056492	AF056492 Mus muscu
4	1070.8	89.7	1194	10 AF302842	AF302842 Rattus no
5	814.4	68.2	1182	6 AR221261	AR221261 Sequence
6	814.4	68.2	1182	6 AX250709	AX250709 Sequence
7	814.4	68.2	1218	6 AR221262	AR221262 Sequence
8	814.4	68.2	1257	6 AX278168	AX278168 Sequence
9	814.4	68.2	1408	6 AX278166	AX278166 Sequence
10	814.4	68.2	1544	9 AF248242	AF248242 Homo sapi
11	814.4	68.2	1730	9 AF259500	AF259500 Homo sapi
12	814.4	68.2	2747	9 AF259501	AF259501 Homo sapi
13	814.4	68.2	2772	9 AF247042	AF247042 Homo sapi
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15	542	45.4	1500	9 BC033577	BC033577 Homo sapi
16	498.4	41.7	568	10 AF259502	AF259502 Rattus no
17	392	32.8	181489	10 AC120557	AC120557 Mus muscu
18	392	32.8	223092	2 AC147519	AC147519 Mus muscu
19	340.8	28.5	257210	2 AC098622	AC098622 Rattus no

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21	259.4	21.7	3056	10 AF385401	AF385401 Rattus no
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23	249.8	20.9	1632	6 AX319989	AX319989 Sequence
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25	249.8	20.9	1716	9 BC075021	BC075021 Homo sapi
26	249.8	20.9	2065	6 AX411765	AX411765 Sequence
27	249.8	20.9	2402	9 AF385399	AF385399 Homo sapi
28	249.8	20.9	2484	9 AF385400	AF385400 Homo sapi
29	249.8	20.9	2730	9 AF279890	AF279890 Homo sapi
30	248.2	20.8	1455	6 CQ718922	CQ718922 Sequence
31	248.2	20.8	1644	6 BD169901	BD169901 Novel pot
32	235.2	19.7	3187	10 AF325671	AF325671 Rattus no
33	235.2	19.7	3291	10 AF385402	AF385402 Rattus no
34	234.8	19.7	174562	2 AC005848	AC005848 Homo sapi
35	233.8	19.6	1674	4 AY553324	AY553324 Oryctolag
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38	229.2	19.2	1993	6 AX018706	AX018706 Sequence
39	229.2	19.2	1993	6 BD140671	BD140671 Novel mam
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43	229.2	19.2	3228	10 BC062094	BC062094 Mus muscu
44	229.2	19.2	3580	6 BD273739	BD273739 Method fo
45	229.2	19.2	3580	10 MM073488	U73488 Mus musculu

## ALIGNMENTS

RESULT 1	AX018705	AX018705	1794 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	Sequence 1 from Patent WO9945108.					
DEFINITION	AX018705					
ACCESSION	AX018705.1	GI:10042825				
VERSION						
KEYWORDS	Mus sp.					
SOURCE	Mus sp.					
ORGANISM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1					
AUTHORS	Pink, M., Honore, E., Duprat, F., Lesage, F. and Lazdunski, M.					
TITLE	Novel mechanically sensitive mammal potassium channel family activated by polyunsaturated fatty acids and their use particularly for screening medicines					
JOURNAL	Patent: WO 9945108-A 1 10-SEP-1999;					
FEATURES	FINK MICHEL (FR); HONORE ERIC (FR); DUPRAT FABRICE (FR); LESAGE FLORIAN (FR); CENTRE NAT RECH SCIENT (FR); LAZDUNSKI MICHEL (FR)					
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## ORIGIN

Query Match 100.0%; Score 1194; DB 6; Length 1794;  
Best Local Similarity 100.0%; Pred. No. 6.1e-259;  
Matches 1194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCTCTAGTGTTCAGGCTCTGAGAGAGCTCTCAGAGCAGAGCTCAGAGAAATGGAT 120  
Db GCTCTAGTGTTCAGGCTCTGAGAGAGCTCTCAGAGCAGAGCTCAGAGAAATGGAT 403  
QY 121 CATGGCCGAGCAGCAGTCTCTGAGGAGCAGTCTCTGAGGAGCAGAGAGCTCTGAGGAT 180  
Db CATGGCCGAGCAGCAGTCTCTGAGGAGCAGTCTCTGAGGAGCAGAGAGCTCTGAGGAT 463  
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Db TTCAATCAAGCTCTCTGTTGAAGCCCTGGAGGGGGCGCAACCCAGAAACAGCTGGACC 523  
QY 241 AATAGCAGCAACCACTCATCAGCTTGAACCTGGGAGCGCCCTCTCTTTTCTCGGGACC 300  
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QY 301 ATCATCACTACCATCGGCTATGCAATATAGTCTTACACACAGATCGCGGCTCTCTTT 360  
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QY 361 TGTATCTTCTATGCACTGTGGGATCCCACTGTTGGGATGCTGCTGGCGGAGTCCGG 420  
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QY 421 GACCGGTGGGCTCTCTCTGCGCGGGGATCGGCCACATCGAAGCAATCTTCTTGAAG 480  
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QY 481 TGGCATGTGCCACCGGGCTGGTGAAGTCTGTCCGAGTGTCTTCTGCTGATCGGC 540  
Db TGGCATGTGCCACCGGGCTGGTGAAGTCTGTCCGAGTGTCTTCTGCTGATCGGC 823  
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QY 721 TTGTTTGGCTAGCCTACTTCTGCTCAGTGTCTCACCCTGAGCTTTGGTGGAGCA 780  
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QY 781 GTGTCCCGCGAACTCTGGGAGAGATGGTGGCTTAACGCGACAGGCTGTAGCTGACC 840  
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QY 901 GAGCAACCACTCTCTGCTCTCTTCTTGGGAGCAGGCTGTGTTGTAGCAGCGCGG 960  
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QY 1081 GAGCGTGGCTGTCCCTGCTCGGCTCTCTGCGGCTCGCGCGAGCCCAACCCATCCAAA 1140  
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RESULT 2  
BD140670 1794 bp DNA linear PAT 18-SEP-2002  
LOCUS Novel mammalian potassium channel families having mechanical  
DEFINITION sensitivity activated by polyunsaturated fatty acid, and method for  
using them particularly for drug screening.  
ACCESSION BD140670.1 GI:23235615  
VERSION JP 2002505102-A/1.  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1794)  
AUTHORS Honore, E., Fink, M., Lazdunski, M., Lesage, F. and Duprat, F.  
TITLE Novel mammalian potassium channel families having mechanical  
sensitivity activated by polyunsaturated fatty acid, and method for  
using them particularly for drug screening  
JOURNAL Patent: JP 2002505102-A 1 19-FEB-2002;  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE  
COMMENT OS Unidentified  
PN JP 2002505102-A/1  
PD 19-FEB-2002  
PF 23-FEB-1999 JP 2000534640  
PI 05-MAR-1998 FR 98/02725  
PI ERIC HONORE, MICHEL FINK, MICHEL LAZDUNSKI, FLORIAN LESAGE, PI  
FABRICE DUPRAT  
PC C12N15/09, A61K31/7088, A61K38/00, A61K39/395, A61K48/  
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PC A61P9/00, A61P21/00, A61P25/00, A61P25/28, C07K14/705, C07K16/28,  
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C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/02, G01N33/ PC  
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CC Topology: Linear;  
CC Novel mammalian potassium channel families having mechanical  
CC sensitivity  
CC activated by polyunsaturated fatty acid, and method for using  
them  
CC particularly for drug screening.  
CC PH Key Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 6.1e-259;  
Matches 1194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCGCAGCACCACATCTCTGGCTCTGCTGGCACTGGTGTCTGCTTACTTTGGTATCTGGG 60  
Db ATGCGCAGCACCACATCTCTGGCTCTGCTGGCACTGGTGTCTGCTTACTTTGGTATCTGGG 343  
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QY 121 CATGGCCGAGCAGCAGTCTCTGAGGAGCAGTCTCTGAGGAGCAGAGAGCTCTGAGGAT 180

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AF056492 1795 bp mRNA linear ROD 20-JUL-1998  
LOCUS Mus musculus TTRAK K+ channel subunit mRNA, complete cds.  
DEFINITION AF056492  
ACCESSION AF056492  
VERSION 1 GI:3329456  
KEYWORDS Mus musculus (house mouse)  
SOURCE  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1795)  
AUTHORS Fink,M., Lesage,F., Duprat,F., Heurteaux,C., Reyes,R., Fosset,M.  
and Lazdunski,M.  
TITLE A neuronal two P domain K+ channel stimulated by arachidonic acid  
and polyunsaturated fatty acids  
JOURNAL ENDO J 17 (12), 3297-3308 (1998)  
MEDLINE 98292450  
PubMed 9628867  
REFERENCE 2 (bases 1 to 1795)  
AUTHORS Fink,M., Lesage,F., Duprat,F., Heurteaux,C., Reyes,R., Fosset,M.  
and Lazdunski,M.  
TITLE Direct Submission  
JOURNAL Submitted (01-APR-1998) Institut de Pharmacologie Moléculaire et  
Cellulaire, CNRS UPR 411, 660 route des Lucioles, Valbonne 06560,  
France  
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ORIGIN	Query Match	Score	DB	Length
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Qy	61	GCTCTAGTGTTCAGGCTCTGGAGCAGCCTCACGAGCAGCAGGCTCAGAGAAAATGGAT	120	
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Qy	241	AATAGCAGCAACCACTCATCAGCTTTGGAAACCTGGGGCAGCGGCTTCTTTTCTCGGGGACC	300	
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QY 841 GGCACTGACAGCGGAGTGAACCGAGTCTGGGCGGAGCGCGCGCGCGCGAGAG 900
Db 1124 GGCACTGACAGCGGAGTGAACCGAGTCTGGGCGGAGCGCGCGCGCGCGAGAG 1183
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Db 1304 GCTCTGATTAACCCAGTGAATCTGGCTTCTCATCGAGTCTCTCAGACAGCGAGT 1363
QY 1081 GAGCGTGGCTGTGCTGCTCTGCGGCTCTCTGCGGCTCGCGCGAGCCCAACCCATCCAA 1140
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QY 1141 AAGCTTTCAGACCCCGGGTCTTGGCGACTCGGAGCAAGCGCGTGGCGGTG 1194
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RESULT 4
AF302842 1194 bp mRNA linear ROD 27-DEC-2001
LOCUS Rattus norvegicus mechanosensitive tandem pore potassium channel
DEFINITION mRNA, complete cds.
ACCESSION AF302842
VERSION AF302842.2 GI:17981766
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1. (bases 1 to 1194)
AUTHORS Kim, Y., Bang, H., Ghatenco, C. and Kim, D.
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TITLE Synergistic interaction and the role of C-terminus in the
activation of TRAAK K+ channels by pressure, free fatty acids and
alkali
JOURNAL Pflugers Arch. 442 (1), 64-72 (2001)
MEDLINE 21268449
PUBMED 11374070
REFERENCE 2 (bases 1 to 1194)
AUTHORS Kim, Y. and Kim, D.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-2000) Physiology, Finch University of Health
Sciences/The Chicago Medical School, 3333 Green Bay Road, North
Chicago, IL 60064, USA
REFERENCE 3 (bases 1 to 1194)
AUTHORS Kim, Y. and Kim, D.
TITLE Direct Submission
JOURNAL Submitted (27-DEC-2001) Physiology, Finch University of Health
Sciences/The Chicago Medical School, 3333 Green Bay Road, North
Chicago, IL 60064, USA
REMARK Sequence update by submitter
COMMENT On Dec 27, 2001 this sequence version replaced gi:14334013.
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Matches 1124; Conservative 0; Mismatches 67; Indels 3; Gaps 1;
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LOCUS AR221261 1182 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 1 from patent US 6426197.  
ACCESSION AR221261  
VERSION AR221261.1 GI:23328170  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1182)  
AUTHORS Duckworth, D.M. and Chapman, C.G.  
TITLE Polynucleotides encoding a human potassium channel  
JOURNAL Patent: US 6426197-A 1 30-JUL-2002;  
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Query Match 68.2%; Score 814.4; DB 6; Length 1182;  
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ACCESSION AX250709  
VERSION AX250709.1 GI:1598447  
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ORGANISM Homo sapiens  
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Lazdunski, M., Lesage, F. and Maingret, F.  
Novel family of mechanically sensitive human potassium channels  
activated by polyunsaturated fatty acids and use thereof  
Patent: WO 0168670-A 1 20-SEP-2001;  
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Query Match 68.2%; Score 814.4; DB 6; Length 1182;  
Best Local Similarity 81.5%; Pred. No. 3.3e-173;  
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ACCESSION AR221262  
VERSION AR221262.1 GI:23328171  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1218)

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DEFINITION	Homo sapiens linear
ACCESSION	AF259501
VERSION	AF259501.1 GI:13925517
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ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Ozaite,A. and Vega-Saenz de Miera,E. Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human two-pore K+ channel gene KCNK4. Chromosomal localization, tissue distribution and functional expression Brain Res. Mol. Brain Res. 102 (1-2), 18-27 (2002) 2 (bases 1 to 2747) Ozaite,A. and Vega-Saenz de Miera,E.C. Direct Submission Submitted (21-APR-2000) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA
REFERENCE	JOURNAL
AUTHORS	REFERENCE
TITLE	AUTHORS
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	JOURNAL

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ORIGIN

Query Match 68.2%; Score 814.4; DB 9; Length 2747;  
Best Local Similarity 81.5%; Pred. No. 3e-173;  
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;  
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601	TTAGAAGCCATCTACTTTGTATAGTAGTCTCTCACCACTGTAGGCTTTGGCGATTATGA	660
726	CTGAGGCCATCTACTTTGTTCATAGTAGCTTACCAACGTTGGGCTTTGGCGACTATGT	785
661	CCGGCGATGGCACCGGGCAGAACTCTCAGCCTACAGCGCTGGTGTGGTCTCGATC	720
786	GCCGGCGGACCCAGGAGGACTCCCGGGCCTATCAGCGCTGGTGTGGTCTCGATC	845
721	TTGTTTGGCTAGCCTACTTCGCTCAGTGTCTCACCACTCGGCAACTGGTTGGCAGCA	780
846	CTGCTCGGCTGGCTTACTTTGGCTCAGTGTCTCACCACTCGGAACTGGCTGCGAGTA	905
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906	GTGTCCCGCGCACTCGGCGAGATGGGGGCTTCAGGCTCAGGCTGCCAGCTGGACT	965
841	GGCAGTGTACAGCGGAGTGTACCGAGCAATCTGGGGCCAGCGCCCGCGCCAGAGAAG	900
966	GGCAGTGTACAGCGCGGTGTACCCAGCAGCGGGGCGCGCCCGCGCGCGGAGAAG	1025
901	GAGCAACCACTCTGGCCCTCTCTTTGGCGGACCGCCTGCTGTGTGAGCCAGCCGGC	960
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1134	GCCCTGGATTATCCAGCGAGAACCTTGGCTTTCATCGACGAGTCTCTCGGATACGCAAGC	1193
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Db	1254	AAGCCGTGGCGCCCGCGCCCGCGCGTCCCGAGACAAAGGCGTGCCTGGTG	1307
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DEFINITION	Homo sapiens tandem pore domain potassium channel TRAAK (KCNK4)		
ACCESSION	AF247042	mRNA, complete cds.	
VERSION	AF247042.1	GI:7576934	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 2772)		
AUTHORS	Gray, A.T.		
TITLE	Assignment of KCNK4 encoding the human potassium channel TRAAK to chromosome 11		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 2772)		
AUTHORS	Gray, A.T.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-MAR-2000) Anesthesia, Room S 261, UC San Francisco, 513 Parnassus Avenue, San Francisco, CA 94143-0542, USA		
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Best Local Similarity	81.5%;	Pred. No. 3e-173;	
Matches	973;	Conservative	0; Mismatches 206; Indels 15; Gaps 2;
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Qy	61	GCTCTAGTGTTCAGGCTCTGGAGCAGCTCTCACGACGAGCTCACGAAGAAATGGAT	120
Db	202	GCCTGTGTTCGGGCTCTGGAGCAGCTCTCACGACGAGCTCACGAAGAAATGGAT	261
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Qy	181	TTCTATCAAGCTCTCTGTGTAAGCCCTGGGAGGGGCGCAAAACCCAGAAACCACTGGACC	240
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Qy	241	AATAGCAGCAACACTCATCAGCTTGGAACTCTGGGAGCGCTCTTTTCTCGGGAGC	300
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Qy	301	ATCATCACTACCATCGGCTATGCAATATAGTCTTTACACACAGATGCCGGGCTCTCTTT	360
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Qy	661	CCCGCGAGTGGCACCGGGCAGAACTCTCCAGCTTACACGCGCTGTGTGTCTTCTGATC	720
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Db	2446	GTGTCCCGCCGCACTCGGGCAGAGATGGCGGCTCTACGGCTCAGGCTGCACGCTGGA	2505
Qy	841	GGCACAGTGCACGGGAGTGCACCGCAGCAATCTGGGCGCAGCGCCCGCCGCCACGAGAAG	900
Db	2506	GGCACAGTGCACGGGCGTGTGACCCACGACGAGCGCGGCGCCCGCCGCCCGCGAGAAG	2565
Qy	901	GAGCAACCACTCTCTGCGCCTCTCTTCTGCGCGCACCGCTCTGTGTGTGTAGCCAGCCGCG	960
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Qy	1021	GCTCTGGATTACCCAGTGAATCTGGCCTTCAATCGACAGAGTCTCTCAGACACGACAGT	1080
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VERSION			
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JOURNAL			





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 14:16:02 ; Search time 652 Seconds

(without alignments)  
9613.204 Million cell updates/sec

Title: US-09-655-272-1\_COPY\_284\_1477

Perfect score: 1194

Sequence: 1 atgcgcagcaccacactct.....gagacaagccgctgcgggtg 1194

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

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10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1194	100.0	1794	2	Aaz10606 cDNA enco
2	814.4	68.2	1182	3	Aaa27105 Human h-T
3	814.4	68.2	1182	4	Aah78636 Human mec
4	814.4	68.2	1218	3	Aaa27106 Human h-T
5	814.4	68.2	1257	6	Aah99922 Nucleotid
6	814.4	68.2	1257	12	Adi27937 Human TWI
7	814.4	68.2	1260	12	Adh51640 Human 123
8	814.4	68.2	1408	6	Aah99921 Nucleotid
9	814.4	68.2	1408	10	Adk52549 Hematolog
10	814.4	68.2	1408	12	Adh51638 Human 123
11	814.4	68.2	1408	12	Adi27935 Human TWI
12	814.4	68.2	2772	10	Aad58498 Human pot
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14	811.4	68.0	3945	8	Abx91950 Human G p
15	811.4	68.0	3996	5	Aas08652 Human cDN
16	811.4	68.0	3996	5	Adq98525 DNA enco
17	811.4	68.0	3996	8	Abx91949 Human G p
18	811.4	68.0	3996	9	Adb48285 Novel hum
19	809.8	67.8	3945	5	Aas11984 Human cDN
20	612.6	51.3	1337	4	Aah78646 Human mec
21	343.4	28.8	1265	4	Abao9473 Human K c

## ALIGNMENTS

RESULT 1

AAZ10606

ID AAZ10606 standard; cDNA; 1794 BP.

AC AAZ10606;

XX 18-NOV-1999 (first entry)

DE cDNA encoding a mechanically sensitive potassium channel protein TRAAK.  
XX Mechanically sensitive potassium channel protein; TRAAK;  
KW polynaturated fatty acid; arachidonic acid; riluzole; heart disease;  
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
KW muscular disease; ds.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 284..1480

FT /\*tag= a

XX WO945108-A2.

XX PD 10-SEP-1999.

XX PF 23-FEB-1999; 99WO-FR000404.

XX PR 05-MAR-1998; 98FR-00002725.

XX PA (CNRS ) CNRS CENT NAT RECH SCI.

XX PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;

XX DR WPI; 1999-551038/46.

XX P-PSDB; AAY30647.

XX PT New mechanically sensitive potassium channel, used to screen for specific  
XX modulators, potential therapeutic agents for heart and nervous system  
XX disorders.  
XX Claim 6; Fig 1; 40pp; French.  
XX The present sequence encodes a mechanically sensitive potassium channel

CC

protein designated TRAAK. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with ischemia or anoxia), abnormalities of hormone secretion and muscular disease. The protein itself may be used to treat these diseases. Antibodies specific for the protein are used to detect it in tissues, also as therapeutic inhibitors or activators

XX SQ Sequence 1794 BP; 348 A; 574 C; 494 G; 378 T; 0 U; 0 Other;

Query Match 100.0%; Score 1194; DB 2; Length 1794;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-313;  
 Matches 1194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GCTCTAGTGTTCAGGCTCTGGAGCAGCTTCAGAGCAGCAGGCTCAGAGAAATGGAT 120  
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Qy 121 CATGGCCGAGACCACTTCTGAGGGACCATCCCTGTGTGAGCCAGAGAGCCTGGAGAT 180  
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Qy 481 TGGCATGTGCAACCGGGGCTGGTGAAGTCTGTCCGAGTGTCTTCTGCTGATCGGC 540  
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Qy 541 TGGCTGTCTTTGCTCCTCACTCTTACCTGTTGTTTCTTACATGAGAGCTGAGCAAG 600  
 Db 824 TGGCTGTCTTTGCTCCTCACTCTTACCTGTTGTTTCTTACATGAGAGCTGAGCAAG 883

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Qy 661 CCGGGCATGGCAGCGGCGAGAACTCTCCAGCCTTACAGCGGCTGGTGTGTTCTGGATC 720  
 Db 944 CCGGGCATGGCAGCGGCGAGAACTCTCCAGCCTTACAGCGGCTGGTGTGTTCTGGATC 1003

Qy 721 TTGTTGGCCCTAGCTACTTCTGGCTCAGTGTCTCACCACCATCGGCAACTGGTGGAGCA 780  
 Db 1004 TTGTTGGCCCTAGCTACTTCTGGCTCAGTGTCTCACCACCATCGGCAACTGGTGGAGCA 1063

Qy 781 GTGTCGCGCGCAACTCGGGCAGAGATGGGGGCTAACCGCAGAGCTGTAGCTGAGCC 840  
 Db 1064 GTGTCGCGCGCAACTCGGGCAGAGATGGGGGCTAACCGCAGAGCTGTAGCTGAGCC 1123

Qy 841 GGCACAGTGCACAGCGGAGTGACCCAGCAACTGGGCCCCAGCGCCCCGCGCAGAGAG 900  
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 Db 1184 GAGCAACCACTCTGCGCTCTCTTTGCGGCAACCGCTGCTGTTGTTGAGCCAGCCGGC 1243

Qy 961 AGGCCCGGCTCCCTCCACCCGAGAGAGTTGAGACTCCGTCGCCGCCACGGCCTCA 1020  
 Db 1244 AGGCCCGGCTCCCTCCACCCGAGAGAGTTGAGACTCCGTCGCCGCCACGGCCTCA 1303

Qy 1021 GCTCTGGAATTACCCAGTGCAGATCTGGCCTTCATGACGAGTCTCAGACAGCAGAT 1080  
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Qy 1081 GAGCGTGGCTGTCCTGCTGCGGCTCTCTGCGGGTCTGCGGCGAGCCCAACCCATCAAA 1140  
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Qy 1141 AAGCCTTCCAGACCCCGGGTCTCTGGCGACTCCGAGACAAGGCCGTGCCGGTG 1194  
 Db 1424 AAGCCTTCCAGACCCCGGGTCTCTGGCGACTCCGAGACAAGGCCGTGCCGGTG 1477

RESULT 2  
 AAA27105  
 ID AAA27105 standard; cDNA; 1182 BP.  
 XX  
 AC AAA27105;  
 XX  
 DT 04-AUG-2000 (first entry)  
 XX  
 DE Human h-TRAAK cDNA sequence #1.  
 XX  
 KW Human; h-TRAAK; potassium channel polypeptide;  
 XX 2P domain potassium channel; neurodegenerative disease; stroke;  
 KW psychiatric disorder; neurological disorder; Gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..1182  
 FT /\*tag= a  
 FT /product= "h-TRAAK protein #1"  
 FT  
 XX  
 PN WO200026253-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 03-NOV-1999; 99WO-GB003634.  
 XX  
 PR 03-NOV-1998; 98GB-00024048.  
 PR 07-OCT-1999; 99GB-00023668.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Chapman CG, Duckworth DM;  
 XX WPI; 2000-365583/31.  
 DR P-PSDB; AAY94425.  
 XX  
 PT Novel isolated h-TRAAK polypeptides belonging to the potassium channel  
 PT family of polypeptides, useful for the diagnosis and treatment of h-TRAAK  
 PT related disorders, e.g. depression and schizophrenia.  
 XX  
 PS Claim 5; Page 21; 35pp; English.  
 XX  
 CC Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK  
 CC polynucleotides from human tissue samples. h-TRAAK polypeptides have  
 CC homology to the 2P domain potassium channel family of polypeptides. The h  
 CC -TRAAK polypeptides and polynucleotides may be used in diagnostic assays  
 CC for conditions related to h-TRAAK imbalance and for identifying agonists

CC	and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and
CC	polynucleotides may also be useful for treatment and prevention (e.g. as
CC	vaccines) of certain diseases, such as pain, psychiatric disorders
CC	including depression and schizophrenia, neurodegenerative disease
CC	including Alzheimer's, stroke and head trauma and neurological disorders
CC	including migraine and epilepsy. The present sequence is human h-TRAAK-1
CC	cDNA sequence #1
XX	
SQ	Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 U; 0 Other;
Query Match 68.2%; Score 814.4; DB 3; Length 1182;	
Best Local Similarity 81.5%; Pred No. 3.2e-210;	
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;	
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Db	1 ATGCGCAGCACCACTCTGGCCCTCTGGCGCTGTGGCTGTGCTTTACTTTGGTGTCTGGT 60
Qy	61 GCTCTAGTGTTCAGGCTCTGGAGCAGCTCACAGCAGCAGGCTCAGAGAAATGAT 120
Db	61 GCCCTGTGTTCGGGGCCCTGGAGCAGCCCAACAGCAGCAGGCCCCAGAGGGAGCTGGG 120
Qy	121 CATGGCCGACACCAAGTTCTGAGGGACCATCCCTGTGTGAGCCAGAGAGCGCTCGAGGAT 180
Db	121 GAGTCCGAGAGAGATTCTTGAGGGCCCATCCGTGTGTGAGCGACACGAGAGCTGGCGCTC 180
Qy	181 TTCACTAAGCTCTGTGTTGAAGCCCTCGGAGGGGGCGCAACCCAGAGAAACCACTCGGACC 240
Db	181 CTCACTAAGGAGTGGCTGATGCCCTGGAGGGGGTGGGACCCAGAGAACCAACTCGACC 240
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Db	658 GCCGCGCGGACCCACGAGCAGACTCCCGCGGCTTATCAGCGGCTGTGTGTGTCTTGTGATC 717
Qy	721 TTGTTTGGCCTAGCCTACTTCGCTCAGTGTCTACCAACCATCGGCAACTGGTTCGAGCA 780
Db	718 CTGCTCGGCTGTGTTACTTCGCTCTAGTGTCTACCAACCATCGGAACTGGCTCGAGTA 777
Qy	781 GTGTCCCGCGAACTCGGGCAGAGATGGTGGCCTTAACGGCACAGGCTGTAGCTGGACC 840
Db	778 GTGTCCCGCGCACTCGGGCAGAGATGGGCGGCTCTACGGCTCAGGCTGCCAGCTGGACT 837
Qy	841 GGCACTGTGACGCGGAGTGACCCAGCAACTGGGCGCCAGCGCCCGCGCCAGAGAG 900
Db	838 GGCACTGTGACGCGGCTGTGACCCAGCAGCGGGGGCGCGCGCCCGCGCGCGGAGAG 897

Qy	901	GAGCAACACTCTGCGCCTCTCTTTTCCCGGCACCGCCTGCTGTGTTGTGAGCCAGCCGCGC	960
Db	898	GAGCAGCACTGC-----TGCTCCACCGCCCTGTCCAGCGCAGCGCCTGCGC	945
Qy	961	AGGCCGCGCTCCCTGCACCGCAGAGAAGGTTGAGACTCCGTCCTCCCGCCACCGGCCTCA	1020
Db	946	AGGCCCGCATCCCTTCGCCCCCGAGAAAGCTCAGCGGCTTCCCGCCACCGGCCTCG	1005
Qy	1021	GCTCTGGATTACCCCACTGAGAACTCTGGCCTTCATCGACGAGTCTCTCAGACACGACAGT	1080
Db	1006	GCCCTGATTATCCACGAGAACTTGGCTTTCATCGACGAGTCTCTCGGATACGACAGC	1065
Qy	1081	GAGCGTGGCTGTGCCCTGCGCTCGGGCTCTCGGGGTGCGCGCCGACCCCAACCCATCCAAA	1140
Db	1066	GAGCGCGGCTTGCCTGCTGCGCGCGCCGAGAGTCTGCGCGCGCCCAATATCCCCCAGG	1125
Qy	1141	AAGCCTTCCAGACCCCGGGTCTCTGGGCGACTCCGAGACAAGGCGCTGCGCGGTG	1194
Db	1126	AAGCCGTGCGGCCCGCGGCCCGGCGTCCCCGAGACAAAGGCGTGGCGGTG	1179
RESULT 3			
AAH78636	ID AAH78636 standard; cDNA; 1182 BP.		
XX	AC	AAH78636;	
XX	DT	10-DEC-2001 (first entry)	
XX	DE	Human mechanically sensitive potassium channel hTRAAK cDNA.	
XX	KW	Human; mechanically sensitive potassium channel; riluzole; TWICK;	
KW	KW	polyunsaturated fatty acid; arachidonic acid; hTRAAK; chromosome 11q13;	
KW	KW	neuronal excitation; muscle excitation; cardiac rhythm; anoxia;	
KW	KW	hormone secretion; cardiac disease; vascular disease; ischemia;	
KW	KW	nervous system disorder; endocrinal disease; muscle disease;	
KW	KW	retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration; ss.	
OS	XX	Homo sapiens.	
XX	XX	Location/Qualifiers	
Key	1.	.1182	
CDS	/*tag=	a	
FT	/product=	"mechanically sensitive potassium channel	
FT	hTRAAK"		
FT	PN	WO200168670-A2.	
XX	PN	20-SEP-2001.	
XX	PF	14-MAR-2001; 2001WO-FR000758.	
XX	PR	14-MAR-2000; 2000FR-00003264.	
XX	PA	(CNRS ) CNRS CENT NAT RECH SCI.	
XX	FI	Lazdunski M, Lesage F, Maingret F;	
XX	DR	WPI; 2001-590037/66.	
XX	DR	P-PSDE; AAG6777.	
XX	PT	New mechanically sensitive potassium channel, useful for treating	
PT	PT	cardiovascular diseases and in drug screening, is activated by	
PT	PT	polyunsaturated fatty acids.	
XX	PS	Claim 4; Page 32-33; 37pp; French.	
XX	CC	The present sequence encodes a human mechanically sensitive potassium	
CC	CC	channel which is activated by polyunsaturated fatty acids (particularly	
CC	CC	arachidonic acid (AA) and by riluzole. The polypeptide is designated	
CC	CC	human TWICK-related AA-activated potassium channel (hTRAAK). The hTRAAK	
CC	CC	gene is located on chromosome 11q13. hTRAAK is involved in regulation of	





PT and cancer.

PS Claim 1; Page 122-124; 124pp; English. XX

This invention relates to a human TWIK-8 (tandem of P domains in a weak inward rectifying K<sup>+</sup> channel)-related potassium channel subunit polypeptide. Applications of the polypeptide include: neurotropic, neuroprotective, antiparkinsonian, antiarteriosclerotic, cytostatic, hypotensive, antidepressant, antimigraine, analgesic, vasotropic, anticonvulsant, neuroprotective, tranquilizer, neuroleptic, in gene therapy, and as a modulator of potassium channel mediated activity in a cell, and is useful in screening assays, detection assays, predictive medicine and in methods of treatment. The polypeptide is useful as a target for developing modulating agents to regulate a variety of cellular processes, and is also useful as query sequence to perform a search against public databases to, for example, identify other family members or related sequences. The polypeptide is useful for treating disorders characterized by insufficient or excessive production of TWIK-8 protein or production of TWIK-8 protein forms which have decreased, aberrant or unwanted activity compared to TWIK-8 wild type protein, e.g., potassium channel associated disorders including central nervous system disorders such as cognitive and neurodegenerative disorders, autonomic function disorders, learning or memory disorders, cardiac disorders, muscular disorders, pain disorders and disorders of cellular growth, differentiation or migration. The polypeptide is useful as immunogen to raise anti-TWIK-8 antibodies, and to screen for drugs, and is also considered useful for producing non-human transgenic animals. This sequence represents the nucleotide sequence for human TWIK-8, which differs to the sequence in AAH99922 since it does not contain the 3' untranslated region

Sequence 1257 BP; 188 A; 443 C; 404 G; 222 T; 0 U; 0 Other;

Query Match	68.2%	Score	814.4	DB	6	Length	1257
Best Local Similarity	81.5%	Pred. No.	3.2e-210				
Matches	973	Conservative	0	Mismatches	206	Indels	15
						Gaps	2

Qy	1	ATGGCGAGCA	CCACAC	TCTCTGGCTCTCGCTGGCA	CTGTGCTGCTTTACTTGGTATCTGGG	60
Db	79	ATGGCAGCA	CCACCGCTCTCTGGCCCTCTGGCG	CTGTGCTTTACTTGGTCTCTGGT	138	
Qy	61	GCTCTAGTG	TTCAGGCTCTGGAGCAGCCTT	CACGAGCAGCAGGCTCAGAGAAATCGAT	120	
Db	139	GCCTCTGTG	TTCGGGGCCCTGGAGCAGCC	CCACAGCAGCAGGCCCCAGAGGGAGCTGGG	198	
Qy	121	CATGGCCGAG	ACAGATTTCTGAGGAGCAATC	CCCTGTGTGAGCCAGAGAGCGCTCGAGGAT	180	
Db	199	GAGGTCGAG	AGAGATTCCTGAGGGCCATCCGTGTGTGAGCAGCAGGAGCTGGGCCCT	258		
Qy	181	TTCATCAAG	CTCTGTGTAAGCCCTGGGAGGGGCG	CAAAACCAGAAACCAAGCTGGAC	240	
Db	259	CTCATCAAG	GAGGTGGCTGATGCCCTGGGAGGGGT	CGGACCCAGAAACCAACTCGAC	318	
Qy	241	AATAGCAGCA	ACCACTCATCAGCTTGGAA	ACTGGGCGAGCGCCTTCTTTTCTTCGGGGAC	300	
Db	319	AGCAACAGC	AGCCAC---TCAGCCTGGGAC	CTGGGACGCGCTTCTTTTCTCAGGGAC	375	
Qy	301	ATCATCACT	ACCATCCGCTATGGCAATATAGT	CTTACACACAGATCGGGCGCTCTCTTT	360	
Db	376	ATCATCACCA	CCATCGGCTATGGCAATGTGGCC	CTGGCAAGATCGGGCGGCTCTTC	435	
Qy	361	TGTATCTT	CATGACCTGGTGGGATCCCACT	GTTCGGGATGCTGTGGGGAGTGGG	420	
Db	436	TGCATCTTT	TATGGCTGTGGGANTTCGGCTGT	TGGGATCTTACTGACAGGGGTGGG	495	
Qy	421	GACCGGTGGG	CTCCTCTCTGCGCCGGGGCATCG	GCCACATCGAAGCAATCTCTTGAAG	480	
Db	496	GACCGGTGG	CTCCCTCGGCCATGGCATCGT	CACATTGAAGCACTTCTTGAAG	555	
Qy	481	TGGCATGTG	CCACCGGGGCTGGTGAAGTCTGT	CCGAGTGTCTTCTCTGCTGATCGG	540	
Db	556	TGGCAGCTG	CCACCGGAGCTAGTAAAGTGTGT	CGGCGATGCTTTTCTTCTGATCGG	615	







QY 781 GTGTCCCGCGAAGTCTCGGCGAGAGATGGTGGGCTTAACGCGACAGGCTGTAGCTGGACC 840  
 DB |||||  
 DB 856 GTGTCCCGCGCACTCGGCGAGAGATGGCGGCTTACGGCTCAGGCTGCGAGTGGACT 915  
 QY 841 GGACAGTGTACGGGAGTGCACCGAGCACTTGGGCGGAGCGCCCGCCGCGCAGAGAG 900  
 DB |||||  
 DB 916 GGACAGTGTACGGGAGTGCACCGAGCACTTGGGCGGAGCGCCCGCCGCGCAGAGAG 975  
 QY 901 GAGCAACCACTCTCTGCGCTCTCTTTGCGCGCACCGCTGCTGTGTGTAGCCAGCGCGC 960  
 DB |||||  
 DB 976 GAGCAGCACTGC-----TGCCTCCACCGGCTTCCAGCGCAGCGCTGGC 1023  
 QY 961 AGGCGCGGCTCCCTGTGCACCGCGAGAGAGTGTAGACTCGTTCGCGCCGCGCAGGCTCA 1020  
 DB |||||  
 DB 1024 AGGCGCGGATCCCTTTCGCGCCCGCGAGAGGCTCAGCGGCTTTCGCGCCGCGCAGGCTCG 1083  
 QY 1021 GCTCTGATTAACCCAGTGAATCGGCTTTCATGACAGAGTCCCTCAGACAGCGAGT 1080  
 DB |||||  
 DB 1084 GCGCTGATTAATCCAGCGAGAACCTGGCTTTCATGACAGAGTCCCTCGGATACGAGAGC 1143  
 QY 1081 GAGCGTGGCTGTGCGCTCGGCTCTCGGGTCTCTCGGGTCCGCGCGAGCCCAACCCATCCAAA 1140  
 DB |||||  
 DB 1144 GAGCGGCTGTGCGGCTGCGCGCGCGCGAGAGTCCGCGCGCCGCGCCCAATCCCGCAGG 1203  
 QY 1141 AAGCCTTCCAGACCCCGGGTCTCTGGCGACTCCGAGACAAAGCCCGTCCCGGTG 1194  
 DB |||||  
 DB 1204 AAGCCGTGCGGCGCGCGCGCGCGCGTCCCGAGACAAAGCGGTGCGCGGTG 1257

## RESULT 8

AAH99921

ID AAH99921 standard; cDNA; 1408 BP.

AC AAH99921;

XX

XX

DT 25-JAN-2002 (first entry)

DE

XX Nucleotide sequence of human TWIK-8 receptor channel.

XX Human; potassium channel; transmembrane domain; TWIK; TWIK-8;

XX Tandem of P domain in a Weak Inward rectifying K<sup>+</sup> channel; K<sup>+</sup>;

XX central nervous system disorder; cardiovascular disorder;

XX potassium channel mediated disorder; Alzheimers disease;

XX Parkinsons disease; multiple sclerosis; Picks disease;

XX neurodegenerative disorder; Lewy diffuse body disease; senile dementia;

XX Huntingtons disease; movement disorder; epilepsy; AIDS related dementia;

XX Gilles de la Tourettes syndrome; amyotrophic lateral sclerosis;

XX progressive supranuclear palsy; Jakob-Creutzfeldt disease;

XX autonomic function disorder; neuropsychiatric disorder; phobia;

XX bipolar affective disorder; ss; nootropic; neuroprotective;

XX antiparkinsonian; antiarteriosclerotic; cytostatic; hypotensive;

XX antidepressant; antimigraine; analgesic; vasotrophic; anticonvulsant;

XX neuroprotective; tranquilizer; neuroleptic; cancer;

XX learning and memory disorder; cell proliferation disorder.

XX Homo sapiens.

OS

XX

PH Key Location/Qualifiers

FT CDS 84..1343

FT /\*tag= a

FT /product= "human TWIK-8"

XX

XX WO200177329-A2.

XX

XX 18-OCT-2001.

XX

XX 06-APR-2001; 2001WO-US011301.

XX

XX 07-APR-2000; 2000US-0195734P.

XX

XX (MILL-) MILLENIUM PHARM INC.

XX

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XX

XX

XX

XX

Glucksmann MA;

WPI; 2002-010911/01.

P-PSDB; AAG78406.

XX

PT Novel isolated 12303, a human tandem of P domains in a weak inward

PT rectifying potassium channel-related potassium channel subunit

PT polypeptide useful for treating Alzheimer's disease, restenosis, migraine

PT and cancer.

XX

PS Claim 1; Fig 1; 124pp; English.

XX

CC This invention relates to a human TWIK-8 (tandem of P domains in a weak

CC inward rectifying K<sup>+</sup> channel)-related potassium channel subunit

CC polypeptide. Applications of the polypeptide include: nootropic,

CC neuroprotective, antiparkinsonian, antiarteriosclerotic, cytostatic,

CC hypotensive, antidepressant, antimigraine, analgesic, vasotrophic,

CC anticonvulsant, neuroprotective, tranquilizer, neuroleptic, in gene

CC therapy, and as a modulator of potassium channel mediated activity in a

CC cell, and is useful in screening assays, detection assays, predictive

CC medicine and in methods of treatment. The polypeptide is useful as a

CC target for developing modulating agents to regulate a variety of cellular

CC processes, and is also useful as query sequence to perform a search

CC against public databases to, for example, identify other family members

CC or related sequences. The polypeptide is useful for treating disorders

CC characterised by insufficient or excessive production of TWIK-8 protein

CC or production of TWIK-8 protein forms which have decreased, aberrant or

CC unwanted activity compared to TWIK-8 wild type protein, e.g., potassium

CC channel associated disorders including central nervous system disorders

CC such as cognitive and neurodegenerative disorders, autonomic function

CC disorders, learning or memory disorders, cardiac disorders, muscular

CC disorders, pain disorders and disorders of cellular growth,

CC differentiation or migration. The polypeptide is useful as immunogen to

CC raise anti-TWIK-8 antibodies, and to screen for drugs, and is also

CC considered useful for producing non-human transgenic animals. This

CC sequence represents the nucleotide sequence for human TWIK-8

XX

SQ Sequence 1408 BP; 204 A; 500 C; 459 G; 245 T; 0 U; 0 Other;

QY

Best Match 68.2%; Score 814.4; DB 6; Length 1408;

QY

QY

QY

QY

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QY

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QY

QY

QY

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QY

QY

QY

QY

QY



342	CTCATCAAGGAGTGGCTGATG	CTCCCTGGGAGGGGGTCCGAC	CCAGAAACCACTCGACC	401
241	AATAGCAGCAACCACTCAT	CAGCTTGGAACCTTGGGCA	CGCGCTTCTTTTCTCGGGACC	300
402	AGCAACAGCAGCCAC---	TCAGCTGGGACCTTGGGCA	CGCGCTTCTTTTCTCAGGGACC	458
301	ATCATCTACTACCATCGGCT	ATGGCAATATAGTCTTACAC	ACAGATCCGGGGGCTCTTTT	360
459	ATCATCACCACTATCGGCT	ATGGCAATATGGCCCTTGGCA	CAGATGCGCGGCGCTCTTC	518
361	TGTATCTTCTATGCACTG	TGGGATCCCACTGTTTGGGAT	GTCTGCGCGGAGTCCGG	420
519	TGCACTTTTATGGCGT	TGGGATTCGCTGTTTGGGAT	CTTACTTGGCAGGGTCCGG	578
421	GACCGGTGGGCTCTCTCT	TCGCGCGGGGCATCGGCCA	CTCAATCGAACAATCTTTTGAAG	480
579	GACCGGTGGGCTCTCCCT	CGGCAATGGCATCGGTCA	CTTGAAGCATCTTCTTGAAG	638
481	TGCAATGTCACCGGGGCT	GTTGAGAATCTGTCGCGAGT	GTCTTCTCTCTGATCGGC	540
639	TGGCACTGTCACCGGAGCT	AGTAGTAGTCTGTCGGCGAT	GTCTTCTCTGATCGGC	698
541	TGCTGTCTTTTGTCTCACT	CTCTACCTCTCGTGTCTCT	TACATGGAGAGCTTGAGCAAG	600
699	TGCCTGTCTTTGTCTCTA	CGCCACGTTTGGTGTCTG	CTATATGGAGAGCTTGAGCAAG	758
601	TTAGAAGCCATCTACTTT	TGTATATAGTCACTCTACCA	CTGTAGGCTTTTGCGATATATGTA	660
759	CTGAGGCCATCTACTTT	TGTATAGTGAAGCTTACCA	CGTGGGCTTTGGCGATATGTG	818
661	CCGGCGATGGCACCGGGCA	MACTCTCAGCCTTACCAGCG	CTGGTGTGGTCTTGATC	720
819	GCGGCGCGGACCCACGCA	GGAGCTCCCCGGCCTTAT	CAGCGCTGTGTGTCTTGATC	878
721	TTGTTTGGCCTTAGCTACT	TTTCGCTCTCAGTGTCTACA	CCACCATCGGCAACTGGTTGCCAGCA	780
879	CTGCTCGGCTTGGCTTACT	TTCGCTCTCAGTGTCTACA	CCACCATCGGGAATCGCTGCGAGTA	938
781	GTGTCCCGCGAATCCGGG	CAGAGATGGGTGGCTTAAC	CGGCACAGGCTGTAGCTGAGCC	840
939	GTGTCCCGCGCACTCGGG	CAGAGATGGGGCGCTTCA	CGGCTCAGGCTGCGAGCTGAGCT	998
841	GGCACAGTGACGGCGAGTG	ACCCAGGAACTGGGCGCAG	CGCGCCCGCGCCAGCAGAGAAG	900
999	GGCACAGTGACGGCGGCT	GACCCAGCAGCGGGCGCG	CGCGCCCGCGCCAGGAGAAG	1058
901	GAGCAACCACTCTCTG	CTCTCTTTCGCGCACCGCT	GTGTGTGTAGGACAGCCCGGC	960
1059	GAGCAGCACTGC-----	-----TGCTCCACCGCCCT	GTCCAGCGAGCCGCTGGGC	1106
961	AGGCGCGGCTCCCTGTG	CACCGCAGAGAAGTTGAG	ATCTCGTCCCGCCACAGGCTCTCA	1020
1107	AGGCGCGGATCCCTT	CGCCCGCCGAGAAAGCT	CAGCGGCTTCCCGCGCCACAGGCTCTCG	1166
1021	GCCTGTGATTACCCCACT	GTAGAACTCGGCTTCACT	CAGCAGTCTCTCAGACACGACAGT	1080
1167	GCCCTGTGATTATCCAC	GAGAACTCTGGCTTCTAT	CAGCAGTCTCTCGATATCGCAGAC	1226
1081	GAGCGTGGCTGTGCTCT	CGGCTCTCTCGGGGTG	CGCGGCTCTCGACCAACCCATCCAAA	1140
1227	GAGCGCGGCTGCCGCT	GCCCGCGCCGAGAGT	CGCGCGCCCAATCCCGCCAGG	1286
1141	AAGCCTTCCAGACCCCG	GGGTCTTGGGCGACTCT	CGAGACAAGGCCGTGCGGGT	1194
1287	AAGCCCGTGGGCGCCCG	CGCGCCCGGGCGTCTCC	CGAGACAAGAGCGTTCGCGTG	1340

## RESULT 10

ADH51638

ID ADH51638 standard; cDNA; 1408 BP.

XX  
XX  
XX

AC ADHS

XX

25-MAR-2004 (first entry)

Human 12303 protein cDNA sequence

cytostatic; vasotropic; haemopoietic; respiratory; muscular; immunosuppressive; cardiovascular; antianemic; endocrine; neoplastic; gene therapy; cellular proliferation; blood vessel; platelet; breast; pancreatic; skeletal muscle; immune disorder; inflammatory; endothelial cell; liver; viral neoplasm; endocrine disorder; chromosomal mapping; predicted; ss; 12303.

Homologous proteins.

US2003219806-A1.

27-NOV-2003.

18-MAR-2003;	2003US-003913199;
22-FEB-2000;	2000US-00510706;
07-APR-2000;	2000US-01957340;
31-MAY-2000;	2000US-00583373;
26-JUN-2000;	2000US-0214176P;
08-AUG-2000;	2000US-02634666;
01-SEP-2000;	2000US-0023036P;
19-SEP-2000;	2000US-0233337P;
01-FEB-2001;	2001US-0267076P;
20-FEB-2001;	2001US-00789481;
12-MAR-2001;	2001US-0275107P;
12-MAR-2001;	2001US-0275172P;
06-APR-2001;	2001US-00828035;
26-JUN-2001;	2001US-00991462;
29-AUG-2001;	2001US-00942447;
17-SEP-2001;	2001US-0322983P;
19-SEP-2001;	2001US-00957683;
27-SEP-2001;	2001US-0325854P;
04-DEC-2001;	2001US-0063936P;
31-JAN-2002;	2002US-00062937;
08-MAR-2002;	2002US-00094211;
11-MAR-2002;	2002US-00095139;
17-SEP-2002;	2002US-00245121;
26-SEP-2002;	2002US-00255532;
04-DEC-2002;	2002US-00303804;
04-DEC-2002;	2002US-00309504;

(MILL-) MILLENNIUM PHARM INC.

Glucksmann MA, Curtis RAJ, Lora JM, Galvin KM, Silos-Santiago I;

WPI: 2004-010868/01.

P-PSDB; ADH51639.

New 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063, 52991, 59914, 59291 or 33751 nucleic acid molecule or polypeptide, useful for diagnosing, preventing or treating e.g. proliferative or brain disorders.

Claim 1: SEO ID NO 18: 276pp: English.

This invention relates to novel human DNA sequences (designated 18607, 15603, 69318, 13203, 48000, 52920, 5433, 38554, 57301, 58324, 55063, 52991, 59914, 59901 or 33751) and the proteins encoded by them. The invention may be useful for the development of compounds with a cytostatic, vasotropic, haemostatic, nephrotropic, gastrointestinal-Gen, respiratory-Gen, muscular-Gen, osteopoeitic, antiinflammatory, immunosuppressive, cardiovascular-Gen, hepatotropic, virucide, analgesic, antanaemic, endocrine-Gen, neuroprotective, nootropic or cardiant activity. In addition the sequences may be useful for gene therapy. The

invention may be useful in diagnosing, preventing or treating disorders characterised by aberrant 18607, 15603, 69318, 12303, 48000, 52920, 5433, 39554, 57301, 58324, 55063, 52991, 53914, 59921 or 33751 activity. For example cellular proliferative and/or differentiative disorder, brain disorder, blood vessel disorder, platelet disorder, breast disorder, colon disorder, kidney disorder, lung disorder, ovarian disorder, prostate disorder, pancreatic disorder, skeletal muscle disorder, testicular disorder, hormonal disorder, disorder associated with bone metabolism immune disorder, inflammatory disorder, cardiovascular disorder, endothelial cell disorder, liver disorder, viral disease, pain, metabolic disorder, anaemia, angiogenesis disorder, neoplastic disorder, endocrine disorder, neurological disorder or heart disorder. They may also be used in screening assays, tissue typing, chromosomal mapping, predictive medicine or pharmacogenomics. The present sequence is that of a cDNA which encodes the human 12303 protein of the invention.

XX  
Sequence 1408 BP: 204 A: 500 C: 459 G: 245 T: 0 U: 0 Other;

Query Match	68.2%	Score 814.4	DB 12	Length 1408
Best Local Similarity	81.5%	Prod. No. 3.4e-210		
Matches 973	Conservative	0	Mismatches 206	Indels 15
Gaps				
QY	1	ATGGCGCAGCACACACTCCTGGCTCTGTGTGGACATGTGTGCTGCTTTACTTGGTATCTGGG	60	
DB	162	ATGGCGCAGCACACACCTCTCTGGCCCTGCTGTGGGCTGTGTGCTTGTCTTACTTGTGCTGCTGT	221	
QY	61	GCTCTAGTGTTCAGAGCTCTCGAGCAGCCTCAAGCAGCAGAGGCTCAGAGAAAATGGAT	120	
DB	222	GCCCTGGTGTTCGGGCCCTGGAGCAGCCCAACGAGCAGCAGGCGCCAGAGGAGCTGGGG	281	
QY	121	CATGGCCGAGACCAAGTTTCTGAGGAGACCATCCCTGTGTGAGCCAGAGAGGCTGTGAGGAT	180	
DB	282	GAGGTCCGAGAGAAATTCCTGAGGGCCCATCCGTGTGTGAGGACCAAGAGCTGGGCCCTC	341	
QY	181	TTTCATCAAGCTCCTGGTTGAAGCCCTGGGAGGGGCGCAAAACCCAGAAACCACTGGAGCC	240	
DB	342	CTCATCAAGGAGGTGGCTGATGCCCTGGGAGGGGTGCGGACCCAGAAACCAACTCGACC	401	
QY	241	AATAGCAGCAACCATCATCAGCTTTGGAACCTGGGCAGGGCCTCTTTTCTCGGGGACC	300	
DB	402	AGCAACAGCAGCCAC---TCAGCCTGGACCTGGGCGAGGCGCTCTTTTCTCGAGGACC	458	
QY	301	ATCANTCATACCATCGGCTATGGCAATATAGTCTTACACAGATGCGGGCGCTCTCTTT	360	
DB	459	ATCATCACACCATCGGCTATGGCAATATGGGCCCTGCGCACAGATGCGGGCGCTCTTC	518	
QY	361	TGTATCTTCTATGCACTGTGGGGATCCCACTGTTTCGGGATGCTGCTGGCGGAGTCGGG	420	
DB	519	TGCNCTTTATGCGCTGTGGGGATTCGCTGTTTGGGATCCTATGCGAGGGGTCTGGG	578	
QY	421	GACCGGCTGGGCTCTCTCTGGCGGGGCGATCGGCCACATCGAGCAATCTTCTTGAGG	480	
DB	579	GACCGGCTGGGCTCTCTCTGGCGGCCATGGCATCGGTGCATTTGAAGCCATCTCTTGAG	638	
QY	481	TGGCATGCGCACCGGGGCTGTGTGAGAAGTCTGTGCGCAGTGTCTTCTCGCTGATCGCG	540	
DB	639	TGGCAGTGGCCACCGGAGCTAGTAAAGATGCTGTGCGCGATGCTTTCTGCTGATCGCG	698	
QY	541	TGGCTGCTTTTGTTCCTCACTCCTACTTCTGTTTCTCCTATCATGAGAGCTGTGAGCAAG	600	
DB	699	TGCTGCTTTTGTCTCAGCGCCACGTTTCTGTTCTATATGAGGACTGTGAGCAAG	758	
QY	601	TTAGAAGCCATCTACTTTGTATTAGTACTCTCACCACCTGTAGGCTTTGCGCATATGTA	660	
DB	759	CTGGAGGCCATCTACTTTGTCTAGTGAAGCTTTACCAACCGTGGGCTTTGGCGACTATGTG	818	
QY	661	CCCGGGATGGCACCGGGCAGAACTCTCAGACCTTACAGCCGCTGTGTGTTTCTGGATC	720	
DB	819	GCCGGCGCGGACCCGAGGAGGACTCCCGGCCCTATCAGCCGCTGTGTGTTTCTGGATC	878	
QY	721	TTGTTTGGCCTAGCCTACTTTCGCTCAGTGTCTCAGCCNATCGGCAACTGGTGTGCGAGCA	780	
DB	879	CTGCTCGGCTCGGCTTACTTTCGCTCAGTGTCTCAGCCATCGGCAACTGGTGTGCGAGTA	938	





/product= "Human potassium channel"  
/note= "The CDS is referred to as SEQ ID NO:45 in the  
specification"

WO2003061573-A2.

31-JUL-2003.

16-JAN-2003; 2003WO-US001450.

18-JAN-2002; 2002US-0349511P.

28-FEB-2002; 2002US-0360500P.

15-MAR-2002; 2002US-0365041P.

19-APR-2002; 2002US-0374063P.

14-AUG-2002; 2002US-0403468P.

21-SEP-2002; 2002US-0414262P.

PR 21-OCT-2002; 2002US-0419986P.

PR 05-NOV-2002; 2002US-0423809P.

PR 26-NOV-2002; 2002US-0429797P.

(MILL-) MILLENNIUM PHARM INC.

Silos-Santiago I, Karicheti V;

WPI; 2003-598705/56.

DR P-PSDB; AAE38597.

Identifying a compound for treating urological disorders, for example urinary incontinence by assaying the ability of the compound to modulate the nucleic acid expression or polypeptide activity.

Disclosure; Page 194-195; Opp; English.

The present relates to a method for identifying a compound for treating urological disorders e.g., urinary incontinence including overactive/oversensitive bladder, overflow urinary incontinence, stress urinary incontinence caused by dysfunction of the bladder, urethra or central peripheral nervous system, prostatitis, benign prostatic hyperplasia, cancer of the prostate or kidney disorders. The method is also useful for modulating hyperplasia in a cell and treating a subject having a urological disorder. The invention is also used in gene therapy. The present sequence is human potassium channel, KCNK4 DNA

Sequence 2772 BP; 521 A; 911 C; 868 G; 472 T; 0 U; 0 Other;

Query Match 68.2%; Score 814.4; DB 10; Length 2772;

Best Local Similarity 81.5%; Pred. No. 4.5e-210;

Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;

1 ATGCGGAGCAGCAGCTCTGCTGCTGGCAGCTGGTGGTCTTACTTGGTATCTGGG 60

142 ATGCGGAGCAGCAGCTCTGCTGCTGGCAGCTGGTGGTCTTACTTGGTATCTGGT 201

61 GCTCTAGTCTTCCAGGCTCTGGAGCAGCTCTACAGAGCAGAGGCTCAGAGAAATGGAT 120

202 GCCTGTGTCTCGGSCCTCTGGAGCAGCCACAGCAGCAGCGCCACAGAGGAGCTGGG 261

121 CATGGCCGAGCAGCTTCTGGAGGACATCTCTGTGAGCCAGAGAGCTCGAGGAT 180

262 GAGGTCGAGAGAGTCTCTGAGGCGCCATCTCGTGTGAGGAGCAGAGAGCTGGGCTC 321

181 TTCTCATGCTCTCTGCTTGAAGCCCTGGAGGAGGCGGCAAAACCCAGAAACAGCTGGAC 240

322 CTCTCATGAGAGTGTGCTGATGCTCTGGAGGAGGCTGGGACCCAGAAACCACTCGACC 381

241 AATGAGCAGCAACCATCTCAGCTTGAACCTGGGAGGCGCTTCTTTTCTCGGGGACC 300

382 AGCAACAGCAGCCAC---TCAGGCTGGGAGGCGCTTCTTTTCTCAGGAGACC 438

301 ATCATCACTACCATCGGCTATGCAATATAGTCTTACACACAGATGCGGGGCTCTCTTT 360

439 ATCATCACTACCATCGGCTATGCAATATAGTGTGGCCCTCGGCACAGATGCGGGGCGCTCTTC 498

361 TGTATCTTCTATGCACTGTGTGGGATCCCACTGTTGCGGATGCTGTCGCGGAGTCGGG 420  
499 TGTATCTTCTATGCGCTGTGTGGGATTCGCTGTTTGGGATCTCTACTGCGAGGGTCGGG 558  
421 GACCGGCTGGGCTCCTTCTGTGCGCGGGGATTCGGGACATCGAAGCAATCTTCTTGAAG 480  
559 GACCGGCTGGGCTCCTCCTGTGCGCATGCGTCAATTAAGCCATCTTCTTGAAG 618  
481 TGGCATGTGCACCGGGGCTGTGAAGTCTCTCCGAGTGTCTTCTTCTGTGATCGGC 540  
619 TGGCATGTGCACCGGAGCTAGTAAGAGTCTGTGCGGATGCTTCTTCTGTGATCGGC 678  
541 TGCCTGCTCTTGTGCTCACTCTTACCTTCTGTTTCTTACATGAGAGCTGGAGCAAG 600  
679 TGCCTGCTCTTGTGCTCACTCTTACCTTCTGTTTCTTATATGAGAGCTGGAGCAAG 738  
601 TTAGAAGCATCTACTTGTGTATAGTACCTTACCACTCTAGGCTTTGGCGGATTAATGA 660  
739 CTGAGAGCCATCTACTTGTGTATAGTACCTTACCACTCTAGGCTTTGGCGACTAATGA 798  
661 CCGGCGATGCGACCGGCGAGAACTCTCCAGCCTTACCAGCGCTGTGTGTCTTGTGATC 720  
799 GCGGCGGAGACCCAGGAGGACTCTCCCGGCTTATCAGCGCTGTGTGTCTTGTGATC 858  
721 TTGTTTGGCTTACCTTCTGCTCTAGTCTACCACTCTGCGCACTGTTGCGGAGCA 780  
859 CTGCTGGGCTTGGCTTACTTCTGCTCTAGTCTACCACTCTGCGCACTGTTGCGGAGTA 918  
781 GTGTCCCGCGAATCTCGGCGAGAGATGGTGGCTTAAACGGCACAGGCTGTAGCTGAGC 840  
919 GTGTCCCGCGGACTCTCGGCGAGAGATGGGCGGCTTACGGCTCAGGCTGAGCTGAGCT 978  
841 GGCACAGTGACAGCGGAGTGACCCAGCGAACTGGGCGCAGCGCGCGCGCGCAGAGAG 900  
979 GGCACAGTGACAGCGGAGTGACCCAGCGAGCGCGCGCGCGCGCGCGCGCGAGAG 1038  
901 GAGCAACACTCTCTGCTCTCTTTCGCGCAGCGCTGCTGTGTTGAGCCAGCGCGCG 960  
1039 GAGCAGCCACTGCT 1086  
961 AGGCGCGGCT 1020  
1087 AGGCGCGGCT 1146  
1021 GCTCTGATATCCAGTGAGATCTGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080  
1147 GCGCTGATATCCAGCGAGAACTTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1206  
1081 GAGCGTGGCTGTGCT 1140  
1207 GAGCGCGGCTGTGCT 1266  
1141 AAGCCTTCCAGACCCCGGGTCTCTGGCGACTTCCGAGACAGCGCGTGGCGGTG 1194  
1267 AAGCCTTCCAGACCCCGGGTCTCTGGCGACTTCCGAGACAGCGCGTGGCGGTG 1320

RESULT 13

ADP21365

ID ADP21365 standard; DNA; 2772 BP.

XX AC ADP21365;

XX AC ADP21365;

DT 09-SEP-2004 (first entry)

DE Gene KCNK4 for screening for cardiac therapeutic preparation.

XX ds: cardiant; gene therapy; cardiac therapeutic preparation;

XX beta-adrenergic receptor antagonist; endothelial receptor antagonist;

XX calcium channel antagonist; phosphodiesterase inhibitor;

XX angiotensin converting enzyme inhibitor; heart failure.

XX Homo sapiens.







Db 2734 GAGCGGGTGCCTGCCCCCGCGCGCGAGAGGTGCGCGCCCAATCCCCCAGG 2793  
Qy 1141 AAGCCTTCCAGAGCCCGGGGTCTGGGCGACTCCGAGACAAGGCCCGTGCCG 1191  
Db 2794 AAGCCCGTGGCGCCCGCGCGCGCGCGTCCCCCGAGACAAAGGCGTGCCG 2844

Search completed: February 2, 2005, 17:34:59  
Job time : 657 secs

Query Match	68.2%	Score 814.4	DB 4	Length 1182
Best Local Similarity	81.5%	Pred. No. 7.9e-219		
Matches 973; Conservative	0	Mismatches 206	Indels 15	Gaps 2
Qy	1	ATGCGCAGCACCACACTCCTGGCTCTGCTGGCACTGGTGTCTGTTTACTTGGTATCTGGG	60	
Db	1	ATGCGCAGCACCACAGCTCTCGGCCCTGCTGGCGCTGGTCTTGTCTTTTACTTGGTGTCTGGT	60	
Qy	61	GCTCTAGTGTTCAGGCTCTGGAGCAGCCTTCACGACGACGAGGCTCAGAGAAAAATGAT	120	
Db	61	GCCTGTGTTCGGGCCCTGGAGCAGCAGCCCAAGCAGCAGCAGGCGCAGAGGAGCTGGG	120	
Qy	121	CATGGCCGAGACCAAGTTTCTGAGGGACCATCTCTGTGTGAGCCAGAGAGCCTCGAGGAT	180	
Db	121	GAGGTCGAGAGAAATTCCTGAGGGCCCATCTCCGTGTGTGAGCGACACGAGGAGCTGGGCGTC	180	
Qy	181	TTTCATCAAGCTCCTGGTTGAGGCCCTCGGAGGGGGCGCAACCCAGAGAAACCACTGGAC	240	
Db	181	CTCATCAAGAGGTGGCTGATGTCCTGGAGGGGGTGGGACCCAGAGAAACCACTCGACC	240	
Qy	241	AATAGCAGCAACCACTCATCAGCTTGGAACTGGGCAGCGCCTTCTTTTTTCTCGGGGACC	300	
Db	241	AGCAACAGCAGCCAC---TCAGCTGGGACCTGGCAGCGCCTCTTTTTTCTCAGGGACC	297	
Qy	301	ATCATCACTACCAATCGGCTATGGCAATATAGTCTTTACACAGAGTCGGGGCGTCTCTTT	360	
Db	298	ATCATCACCACTCGGCTATGGCAATGTGGCCCTCGGCACAGATGCGGGCGCTCTTC	357	







RESULT 4		US-09-799-451-432		; Sequence 432, Application US/09799451	
		; Patent No. 6783969			
		; GENERAL INFORMATION:			
		; APPLICANT: Tang, Y. Tom			
		; APPLICANT: Zhou, Ping			
		; APPLICANT: Goodrich, Ryle			
		; APPLICANT: Asundi, Vinod			
		; APPLICANT: Ren, Feiyan			
		; APPLICANT: Zhang, Jie			
		; APPLICANT: Xue, Aidong J.			
		; APPLICANT: Zhao, Qing A.			
		; APPLICANT: Wang, Jian-Rui			
		; APPLICANT: Ma, Yuning			
		; APPLICANT: Yamazaki, Victoria			
		; APPLICANT: Chen, Rui-hong			
		; APPLICANT: Wang, Zhiwei			
		; APPLICANT: Wang, Dunrui			
		; APPLICANT: Yang, Yonghong			
		; APPLICANT: Wehrman, Tom			
		; APPLICANT: Ghosh, Reena			
		; APPLICANT: Drmanac, Radoje T.			
		; TITLE OF INVENTION: No. 6783969el Nucleic Acids and			
		; TITLE OF INVENTION: Polypeptides			
		; FILE REFERENCE: 803			
		; CURRENT APPLICATION NUMBER: US/09/799,451			
		; CURRENT FILING DATE: 2001-03-05			
		; NUMBER OF SEQ ID NOS: 948			
		; SOFTWARE: PE_FL_genes Version 2.0			
		; SEQ ID NO 432			
		; LENGTH: 2730			
		; TYPE: DNA			
		; ORGANISM: Homo sapiens			
		; FEATURE:			
		; NAME/KEY: CDS			
		; LOCATION: (473)..(2086)			
		US-09-799-451-432			
		Query Match 20.9%; Score 249.8; DB 4; Length 2730;			
		Best Local Similarity 57.5%; Pred. No. 4.2e-60;			
		Matches 493; Conservative 0; Mismatches 352; Indels 12; Gaps 2;			
Qy	1	ATGCGCAGCACACACTCTGGCTCTGCTGCACTGGTGTCTTACTTGTGTTATCTGGG 60			
Db	671	ATGAGTGGAGACGGTGTGGCCATCTTTGTGTTGTGGTCTTACCTTGTCACTGGC 730			
Qy	61	GCTCTAGTGTTCAGGCTCTGGAGCGCTCAAGCAGCAGCGGCTCAGAGAAATGGAT 120			
Db	731	GGTCTTGTCTTCGGGCATTGGAGCAGCCCTTTGAGAGCAGCCAGAGAAATACCATGCC 790			
Qy	121	CATGCCAGACCACTTCTGAGGACCATCCCTGTGTGAGCAGAGAGAGCTGGAGAT 180			
Db	791	TGGAGAGGCGGAATTCCTCGGGATCATCTGTGTGAGCCCGCAGGAGCTGGACG 850			
Qy	181	TTCAATCAAGCTCCTGTGTGAAGCCCTGGGAGGGGCGCAACCCAGAGAAACAGCTGGACC 240			
Db	851	TGTATCAGCATGCTCTTGTATGCTGACAAATGGGAGTCACTCCAAATAGGAAACTCTTCC 910			
Qy	241	AATAGCAGAACCACTCATAGCTTGGAACTGGGAGCGCTTCTTTTCTCGGGACC 300			
Db	911	AACACAGCAGCCAC-----TGGGACCTCGCAGTGCCTTTTCTTTTGTGGAACT 961			
Qy	301	ATCATCACTACCATCGGCTATGGCAATATAGTCTTACACAGATGCGGGCGTCTCTTT 360			
Db	962	GTATTACGACCAATAGGTAATGGAAATATGCTCGAGCATGAGGAGGCAAAATCTTT 1021			
Qy	361	TGTATCTTCTATGCACTGGTGGGATCCCACTGTTTGGGATGCTGCTGGCGGAGTCGGG 420			
Db	1022	TGATTTTATATGCCATCTTTGGAATTCACACTCTTTGGTCTTATTTGGCTTGGAAATGGA 1081			
Qy	421	GACCGCTGGGCTCTCTCTGCGCGGGGCATCGCCACATCGAAGCAATCTTCTTGAAG 480			
RESULT 5		US-09-236-080-5		; Sequence 5, Application US/09236080	
		; Patent No. 6242217			
		; GENERAL INFORMATION:			
		; APPLICANT: Helen Meadows			
		; APPLICANT: Conrad Chapman			
		; TITLE OF INVENTION: No. 6242217el Compounds			
		; FILE REFERENCE: GP30031			
		; CURRENT APPLICATION NUMBER: US/09/236,080			
		; CURRENT FILING DATE: 1999-01-25			
		; NUMBER OF SEQ ID NOS: 6			
		; SOFTWARE: FastSeq for Windows Version 3.0			
		; SEQ ID NO 5			
		; LENGTH: 1994			
		; TYPE: DNA			
		; ORGANISM: Mus musculus			
		US-09-236-080-5			
		Query Match 19.2%; Score 229.2; DB 3; Length 1994;			
		Best Local Similarity 55.3%; Pred. No. 2.2e-54;			
		Matches 472; Conservative 0; Mismatches 373; Indels 9; Gaps 1;			
Qy	1	ATCGCAGCAGCACACACTCTCGGCTCTGCTGGCACTGGTCTGCTTCTTACTTGTGTATCTGGG 60			
Db	607	ATGAATGAAGAACAGTCTCCAGATTTTCCTGGTGTGCTCTTACTCTTACCTGATCATCGGA 666			
Qy	61	GCTCTAGTGTTCAGGCTCTGGAGCAGCTCTCAGCAGCAGGCTCAGAGAAATGGAT 120			
Db	667	GCCGCGGTGTTCAAGCATTTGGAGCAGCTCAGGAGATTTCCAGAGGACCACTTGTG 726			
Qy	121	CATGGCCGAGACCACTTCTGAGGACCATCCCTGTGTGAGCCAGAGAGCCCTGGAGGAT 180			
Db	727	ATCCAGAGCAGACCTTCTATAGCCAGCATGCTGCTCACTCCACCGAGCTTGGACGAA 786			
Qy	181	TTCATCAAGCTCTCTGTGTGAAGCCCTGGGAGGGGGCGCAACCCAGAAACACAGCTGGACC 240			
Db	787	CTCATCAGCAATATGTGCGAGCAATAACGAGGAGTATATCCCTTAGGAAACAGCTCC 846			
Qy	241	AATAGCAGCAACCACTCATCAGCTTGGAACTGGAGAGCGGCTCTTTTCTCGGGACC 300			

Db 847 AATCAAGTTAGTCAC-----TGGGACCTCGAAGCTCTTTCTTCTTTGCTGGTACT 897  
Qy 301 ATCATCACTACCTCGGCTATGGCAATATAGTCTTTACACAGATGCGGGCGCTCTCTTT 360  
Db 898 GTTATCAACACCATAGGATTTGGAACATCTCCCCAGAACTGAAGTGGAAAAATATTC 957  
Qy 361 TGTATCTTCTATGCACTGTTGGGGATCCCACTGTTGGGATGCTGCTGGGGAGTCGGG 420  
Db 958 TGCATCATCTATGCTTGTGGGAAATTCCTCTCTTTGGCTTTCTACTGCTGGGGTGGT 1017  
Qy 421 GACCGGCTGGGCTCTCTCTGCGCGGGGATCGGCCACATCGAAGCAATCTTCTTGAAG 480  
Db 1018 GATCAGCTAGAACTATATTGGAAGAAGAAATTCGCAAAAGTGAAGACATTTATTAAG 1077  
Qy 481 TGGCATGTGCCACCGGGCTGGTGAAGAGTCTGTCCGCACTGCTCTTCTGCTGATCGGC 540  
Db 1078 TGGAAATGTTAGTCAGACGAAGATTGCTATCATCTCCACCATCATCTTCATCTCTTTGGC 1137  
Qy 541 TGGCTGCTCTTTGCTCACTCTCTACCTTCTGTTCTCTCTACATGAGAGCTGGAGCAAG 600  
Db 1138 TGTGTCTCTTTGCTCTCTCTGCTGCTCTCTCTGCTGCTCATATTCAAGCACATAGAAGGCTGGAGCGC 1197  
Qy 601 TTAGAAGCCATCTACTTTGTTATAGTACTCTCACCCTCTAGGCTTTGGCGATTATGTA 660  
Db 1198 CTGAGAGCTATCTATTGTTGTTATCTCTGAGACCAATGGAATTTGAGACTACGTG 1257  
Qy 661 CCGGGGATGGCCCGGGCGAAGAACTCTCCAGCCCTACCGCGCTGGTGTGTTCTGGATC 720  
Db 1258 GCAGGTGGATCAGACATTGAATCTCGGACTCTACAGCCCTGTGGTGTCTGGATC 1317  
Qy 721 TTGTTTGGCTAGCTACTTCTGCTCTGCTCTCACCACCATCGGCAACTGTTGGCAGCA 780  
Db 1318 CTCGTTGGGCTGGCTACTTTGAGCTGTTCTGAGCATGATTTGGGACTGGCTACGGGTG 1377  
Qy 781 GTCTCCGCGCACTCGGGCAGAGATGGGTGGCTTAACGCAAGCTGCTAGCTGAC 840  
Db 1378 ATCTTAAGAAAGCAAGAAAGAGTGGGAGAGTTTCAAGCCGATGCCGCTGAGTGACA 1437  
Qy 841 GGCACAGTGACAGC 854  
Db 1438 GCCAATGTCAAGGC 1451

## RESULT 6

US-09-236-080-1  
; Sequence 1, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1246  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-236-080-1

Query Match 18.5%; Score 220.8; DB 3; Length 1246;  
Best Local Similarity 55.4%; Pred. No. 4e-52;  
Matches 454; Conservative 0; Mismatches 357; Indels 9; Gaps 1;

Qy 35 TGTGCTGCTTTACTTGTATCTGGGGCTCTAGTGTCCAGGCTCTGGAGCAGCTCAGC 94  
Db 166 TGGTTGCTCTATCTATCTGATCATCGAGCCACCGTGTTCAAAGCATTTGGAGCAGCTCATG 225  
Qy 95 AGCAGCAGGCTCAGAGAAATGATCATGCCGAGACCAAGTTTCTGAGGACCATCCCT 154  
Db 226 AGATTTACAGAGGACACCAATTTGTGATCCAGAAGCAACATTCATATCCCAACATTCCT 285

Qy 155 GTGTGAGCCAGAGAGCCTGGAGGATTTTCAATCAAGCTCTCTGTTGAAGCCCTGGGAGGGG 214  
Db 286 GTGTCAATTCGACGGAGCTGGATGAATCATTCAGCAAAATAGTGGCAGCAATAAATCCAG 345  
Qy 215 GCGCAACCCAGAAACAGCTGGACCAATAGCAGCAACCACTCATCAGCTTTGGAACCTGG 274  
Db 346 GGAATTATACCGTTAGAAACACCTCCAATCAAAATCAGTCAC-----TGGGATTTGG 396  
Qy 275 GAGCGCCCTCTCTTTTCTCGGGACCATCATCACTACCATCGCTATGGCAATATAGTCT 334  
Db 397 GAAGTTCTCTCTTTTCTGCTGGCACTGTTATTACAACCATAGGATTTGGAACATCTCAC 456  
Qy 335 TACACACAGATGCGGGCGCTCTCTTTTGTATCTTTATGACATCTGTGGGGATCCCACTGT 394  
Db 457 CACGACACAGAGCGGCGCAAAATATCTGTATCATCTATGCTTACTTGGGAATTTCCCTCT 516  
Qy 395 TCGGATGCTGCTGGCGGAGTCGGGACGGCTGGGCTGCTCTCTGCGCCGGGATCG 454  
Db 517 TTGGTTTCTCTTGGCTGGAGTTGGAGATCAGCTAGGCACCATATTTTGGAAAAGGAATTG 576  
Qy 455 GCCACATCGAAGCAATCTTTTGAAGTGCATGTGCCACCGGGCTGGTGAGAAAGTCTGT 514  
Db 577 CAAAGTGGAGATAGCTTTATTAGTGGAAATGTTAGTCAGACCAAGATTCGCATCATCT 636  
Qy 515 CCGCAGTCTCTTCTGCTGATGGGCTGCTCTCTTTGTCTCTCACTCTTCTTATAGTACTCA 574  
Db 637 CAACATCATATTTATCTATTTTGGCTGTGACTCTTTGTGGCTCTGCTCGCATCATAT 696  
Qy 575 TCTCTACATGAGAGCTGGAGCAAGTTAGAACCACTCTACTTTGTTATAGTACTCTCA 634  
Db 697 TCAACACACATAGAAGCTGGAGTGCCCTGGAGCCCAATTTATTTTGGTTATCACTTAA 756  
Qy 635 CCACTGTAGGCTTTGGCGATTATGTACCGCGGATGTCACCGGCGAGAACTCTCCAGCCT 694  
Db 757 CAACTATTGGATTTGTGACTAGTTGAGTGGATCCGATATTGAATATCTGACTTCT 816  
Qy 695 ACAGCCGCTGCTGTTCTGATCTTGTGGCTTAGCTTCTGCTCTAGCTTCTGCTCAGTCTCA 754  
Db 817 ATAAGCCTGCTGTTGTTCTGATCTCTTGTAGGGCTTGTCTTACTTTGCTGCTCTGA 876  
Qy 755 CCACCATCGCACTGGTTGGAGCAGTGTCCCGCGAACTCGGCGAGAGATGGGTGGCC 814  
Db 877 GCATGATTGGAGATTGGCTCCGAGTGATATCTAAAGAGCAAAAGAGGTTGGAGAGT 936  
Qy 815 TAAAGGCACAGCTGCTAGCTGACCGCGCACAGTGCAGC 854  
Db 937 TCAGACACACGCTGCTGAGTGAGCAGCCACGTCACAGC 976

## RESULT 7

US-09-336-643A-82  
; Sequence 82, Application US/09336643A  
; Patent No. 6399761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/09/336,643A  
; CURRENT FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82





LENGTH: 1575  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (122)..(1117)  
US-09-431-367B-4

Query Match 10.4%; Score 124.4; DB 4; Length 1575;  
Best Local Similarity 54.5%; Pred. No. 5.3e-25;  
Matches 301; Conservative 0; Mismatches 236; Indels 15; Gaps 2;

QY 226 GAACAGCTGGACCAATACGACCAACCATCATCAGCTTGGAACTGGGCGGCTTC 285  
DB 383 GGAGCCAGCTTCCTCAGCAACACACACAGCATGGGCGCTGGAGCTCGTGGCTCTTC 442  
QY 286 TTTTCTCGGGGACCATCATCATCATCGGCTATGGCAATATAGTCTTACACACAGAT 345  
DB 443 TTCTTTCTGTGCCACCATCATCACCATTTGGCTATGGCAACCTGAGCCCCAACAGATG 502  
QY 346 GCCGGGCTCTCTTTTCTATCTATGCACTGGTGGGATCCCATCTTTCGGGATGCTG 405  
DB 503 GCTGCCGCTCTCTGCACTCTCTTTGGCTTTGGGGATCCCATCAACCTCGTGGTG 562  
QY 406 CTGGCGGAGTCGGGGACGGCTGGCTCTCTCTGGCGGGGCTCGGCCACATCGAA 465  
DB 563 CT-----CAACCGACTGGGCGATCTCATGAGGCGGGTGGCTGGCGGCTCTGGC 610  
QY 466 GCAATCTTCTGAAGTGGCATGTGCCACCGGGGCTGGTGAAGTCTGTCCGAGTGCTC 525  
DB 611 AGCAGCTGGGGGCACTGSCAGGATCTTGACAAAGCGGGTGGCTGGCGGCTCTGGC 670  
QY 526 TTCTGTGTGATCGGCTGCTCTTTGTCTCTACTCTACTCTTCTGTTCTCTCTACATG 585  
DB 671 GCCCTCTCTCGGGCTCTCTGCTCTCTGCTGCTGCAACCGCTGCTCTCTCCCAATG 730  
QY 586 GAGAGCTGGAGCAAGTTAGAGCCATCTACTTTCTTATAGTACTCTCACACTGTAGGC 645  
DB 731 GAGGCTGGAGCTACAGAGGGCTTCTACTTCGCTTCATCCCTTCAGCACCGTGGGC 790  
QY 646 TTTGGCGATTATGACCGCGGATGGCACCGGGGAGA---ACTCTCAGCCTACCAGCG 702  
DB 791 TTGGCGGACTAGCTGATTGGAATGAACCCCTCCAGAGGTACCCACTGTGTACAAAG 850  
QY 703 CTGGTGTGGTCTGATCTTTGGCTAGCCTACTTTCGCTCAGTGTCTCACCACCATC 762  
DB 851 ATGGTGTCCCTGTGGATCTCTTTGGGATGGATGGCTGGCTTGATCACTCAACTCATC 910  
QY 763 GGCAACTGGTG 774  
DB 911 CTCTCCAGCTG 922

RESULT 12  
US-09-561-763-3  
Sequence 3, Application US/09561763  
Patent No. 6684373  
GENERAL INFORMATION:  
APPLICANT: Curtis, Rory A.J. et al.  
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
FILE REFERENCE: MNI-074CP2  
CURRENT APPLICATION NUMBER: US/09/561,763  
CURRENT FILING DATE: 2000-04-29  
PRIOR APPLICATION NUMBER: 09/431,367  
PRIOR FILING DATE: 01-11-1999  
PRIOR APPLICATION NUMBER: US 09/259,951  
PRIOR FILING DATE: 01-03-1999  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1497  
TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1497)  
US-09-561-763-3

Query Match 9.8%; Score 117.2; DB 4; Length 1497;  
Best Local Similarity 51.8%; Pred. No. 5.5e-23;  
Matches 384; Conservative 0; Mismatches 328; Indels 30; Gaps 4;

QY 44 TTTACTTGGTATCTGGGGCTCTAGTGTTCAGGCTCTGGAGCAGCTTCAGCAGCAGG 103  
DB 41 TCTACTTGGCCATCGGGCGGCGATCTTGGAGTCTGGAGGACCCACACTGGAAGAGG 100  
QY 104 CTCAGAAAGAAATGGATCATGGCCGAGACCAAGTTTCTGAGGACCAATCCCTGTGTGAGCC 163  
DB 101 CCAAGAAATCTACTACACAGAAAGTGCATCTGCTCAAGGAGTTCCTCGTGCCTGGGTC 160  
QY 164 AGAGAGCTGGAGATTTTCACTAGCTCTGGTGTGAGCCCTGGAGGGGGCCCAAC 223  
DB 161 AGGAGGGCTGGACAAGATCCTAGAGGTGTATCTGATGCTGACAGGACAGGCTGTGGCCA 220  
QY 224 CAGAAACAGCTGGACCAATAGCAGCAACCACTCATCAGCTTGGAACTGGGCGAGCGCT 283  
DB 221 TCAGAGGAAACAGACCTTCAACAC-----TGGAACCTGGCCCAATGCA 265  
QY 284 TCTTTTCTCGGGGACCATCATCATCATCGGCTATGGCAATATAGTCTTACACAG 343  
DB 266 TGAATTTTGCAGCGACCGCTCATTTACCACTTGGATATGGCAATGTGGCTCTCCCAAGACC 325  
QY 344 ATGCCGGGCTCTCTTTTGTATCTTATGCACTGTGGGATCCCACTGTTCGGGATGC 403  
DB 326 CGCGCGGTGGCTCTCTTGTGTCTTATGTTCTTTCGGGGTGGCTCTGC----- 378  
QY 404 TCCTGGCGGAGTCGGGACCGGCTGGCTCCTCTCTCGCGGGGGCATTCGGCCACATCG 463  
DB 379 --CTGACGTGGATCAGTGCCTTGGGCAAGTTCTTCGGGGGACGTGCCAAGAGAC---TAG 433  
QY 464 AAGCAATCTTTGAGTGGCATGTGCCACCGGGCTGTGAGAGTCTGTCCGAGTGC 523  
DB 434 GGCAGTTCTTACCAAGAGAGGTGTGAGTCTCGGAAAGCGCAGATCATCGTGCAGTCA 493  
QY 524 TCTTCTGCTGATCGGCTCGCTCTTGTCTCTCACTCTCACTCTCTCTCTCTCTCTCTCT 583  
DB 494 TCTTCTGCTGTTGGGGCTCTAGTCCACCTGGTATCCACCTCTCTCTCTCTCTCTCTCT 553  
QY 584 TGGAGAGCTGGAGCAAGTTAGAACCATCTACTTTGTATAGTACTCTCACCCTGTAG 643  
DB 554 CTGAGGGTGGAACTACATCGAGGGCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCT 613  
QY 644 GCTTGGCGATTTATGACCGGGGATGGCACCGGCGAGAACTCTCCAGCC---TACCAGC 700  
DB 614 GCTTGGGTGACTTTGTGGCGGTGTGAACCCAGCGCCAACTACCAAGCCCTGTACCGCT 673  
QY 701 CGCTGCTGTGTTCTGATCTTGTGGCTTAGCCCTACTAGCCCTACTTCCCTCTAGTGTCA 760  
DB 674 ACTTGTGGAGCTCTGGAICTACTTGGGGTGGCTGTCTCCCTTTTGTCTCACTGGA 733  
QY 761 TCGGCAACTGGTTGCGAGCAGT 782  
DB 734 AGGTGAGCATGTTTGTGGAAGT 755

RESULT 13  
US-09-431-367B-3  
Sequence 3, Application US/09431367B  
Patent No. 6670149  
GENERAL INFORMATION:  
APPLICANT: Curtis, Rory A.J.  
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
FILE REFERENCE: MNI-074CP  
CURRENT APPLICATION NUMBER: US/09/431,367B  
CURRENT FILING DATE: 1999-11-01  
PRIOR APPLICATION NUMBER: 09/259,951



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; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1497)
US-09-431-357B-3

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Query Match	9.8%	Score 117.2	DB 4	Length 1497
Best Local Similarity	51.8%	Pred. No. 5.5e-23		
Matches 384	Conservative 0	Mismatches 328	Indels 30	Gaps 4
QY	44	TTTACTTGGTATCTGGGGCTCTAGTGTTCAGAGCTCTGGAGCAGCCTCACGAGCAGCAGG	103	
Db	41	TCCTACTGGCCATCGGGGCGGCATCTTCGAGTGTCTGGAGGCCACACTGAGAGAGG	100	
QY	104	CTCAGAAGAAAATGGGATCATGGCCGAGCAGGTTTCTGAGGGACCAATCCCTGTGTGAGCC	163	
Db	101	CCAAGAAAATACTACTACACACAGAAGCTGCATCTGCTCAAGGAGTTCCTCGTCCTGGGTC	160	
QY	164	AGAGAGCCTCGGAGGATTTTCATCAAGCTCTGTTGAAGCCTTGGGAGGGGGCGCAACC	223	
Db	161	AGAGGGCCTGGACAAAGATCCTAGAGTGTATCTGTATGCTGCAGGACAGGGGTGTGGCCA	220	
QY	224	CAGAAACCAAGCTGGACCAATAGCAGCAACCACTCATCAGCTTGGAACCTGGGACAGCGCCT	283	
Db	221	TCACAGGGAACAGACCTTCAAACAAC-----TGGAACCTGGCCCAATGCAA	265	
QY	284	TCCTTTTCTCGGGACCATCATCACTACCATTCGGCTATGGCAATATAGTCTTTACACAG	343	
Db	266	TGATTTTTCGAGGACCGCTCATTACCACCAATGGATATGGCAATGTGGCTCCCAAGACCC	325	
QY	344	ATSCCGGGCGTCTCTTTTGTATCTCTCATCACTGTGTGGGATCCCACTGTCGGGATGC	403	
Db	326	CCGCGGTCGCCCTCTCTCTGTGTTTTCATGGTCTCTTCGGGGTGCCGCTCTGC-----	378	
QY	404	TGTCGCGGGAGTTCGGGACCGGTGGGCTCCTCTCTGCGCCGGGGCATCGGCCACATCG	463	
Db	379	--CTGACGTGGATCAGTGCCTCGGGCAAGTCTTCGSGGGACGTGCCAAGAGAC---TAG	433	
QY	464	AAGCAATCTTCTTGAAGTGGCATGTGCCACCGGGGCTGGTGAAGTCTGTCTCGCAGTGC	523	
Db	434	GGCAGTTCCTTACCAAGAGAGGTGTAGTCTCGGAGGGCGAGATCACGTGCACAGTCA	493	
QY	524	TCCTTCCTGCTGATCGGCTGCTGCTCTTTCTCTCTCACTCTCTCTCGTGTCTCTCTACA	583	
Db	494	TCCTTCATGCTGTGGGGGCTCTAGTCACCTGTGATCCACCTTCGTATTCATGTGTGA	553	
QY	584	TGGAGAGCTGGACAAAGTTAAGACCAATCTACTTTGTATATAGTGACTCTCACCACTGTAG	643	
Db	554	CTGAGGGTGGAACTACATCGAGGGCCTCTACTACTCTCTTCATCACCATCTCCACCATCG	613	
QY	644	GCTTTGGCGATTATGATCCGGCGATGGCACCGGGCAGAACTCTCCAGCC---TACCAGC	700	
Db	614	GCTTTCGGTGACTTTGTGGCCGGTGTGAACCCCAAGCCCACTACCACGCCCTGTACCGCT	673	
QY	701	CGCTGTGTGGTCTTGATCTGTGTTGGCCCTAGCCTACTTTCGCTCAGTGTCTCACCACTCA	760	
Db	674	ACTTCGTGGAGCTCTGGATCTACTTGGGGCTGCGCCTGGCTGTCCCTTTTGTCACTGGA	733	
QY	761	TCGGCAACTGGTTGGCAGCAGT	782	
Db	734	AGGTGAGCATGTTTGTGGAAGT	755	

## RESULT 14

RESULT 14  
US-09-561-763-1

US-09-561-763-I  
: Sequence 1. Application US/09561763

Sequence I, Application No. 6664373

```

; GENERAL INFORMATION:
; APPLICANT: Curtis, RORY A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MMI-074CE2
; CURRENT APPLICATION NUMBER: US/09/561.763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10) ..(1506)
US-09-561-763-1

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Query Match	9.8%; Score 117.2; DB 4; Length 3452;
Best Local Similarity	51.8%; Pred. No. 8.1e-23;
Matches	384; Conservative 0; Mismatches 328; Indels 30; Gaps 4;
QY	44 TTACTTGGTATCTGGGGCTCTAGTGTTCAGGCTCTGGAGCAGCCTCACGACGAGCAGG 103
DB	50 TCTACTTGGCCATCGGGCGCGGATCTTCAAGTGTCTGGAGGACCACTGGGAAGAGG 109
QY	104 CTCAGAAGAAAATGGGATCATGGCGAGACAGATTTCTGAGGGACCACTCCCTGTGTGAGCC 163
DB	110 CCAAGAAAACACTACTACACACAGAAGCTGATCTGCTCAAGGAGTTCCTCGTCTGGGTC 169
QY	164 AGAAGACCTCGAGGATTTTCATCAGCTCTCTGGTTGAAGCCCTGGGAGGGGGCGCAAC 223
DB	170 AGGAGGGCCTGGACAAGATCCTAGAGTGGTATCTGATGCTGCAGGACAGGGGTGTGGCCA 229
QY	224 CAGAAACCAAGCTGGACCAATAGCAGCAACCACTCATCAGCTTCGAACTTGGACAGCGCT 283
DB	230 TCACAGGAACCAAGACCTTCAAAC-----TGGAACTGGCCCCAATGCAA 274
QY	284 TCTTTTTTCTGGGGACCATCATCACTACCACTCGGCTATGGCAATATAGTCTTTACACAG 343
DB	275 TGATTTTTCAGCGACCGTCATTTACCACCATTGGATATGCAATGTGCTCCCAAGACCC 334
QY	344 ATCCGGGGCGTCTCTTTTGTATCTTCTATGCACTGTGGGGATCCCACTGTTCGGGATG 403
DB	335 CCGCGGTGCGCTCTTCTGTGTTTCTATGGTCTCTTCGGGGTGCCTCTGC----- 387
QY	404 TGTCTGGGGAGTCGGGACCGGCTGGGCTCTCTCTGCGCGGGGATCGGCCACATCG 463
DB	388 --CTGACGTGGATCAGTGCCCTGGCAAGTTCCTTCGGGGACGTGCCAAGAGAC---TAG 442
QY	464 AAGCAATCTTCTTGAAGTGGCATGTGCCACCGGGGCTGGTGAGAAGTCTGTCCGAGTGC 523
DB	443 GGCAGTCTCTTACCAAGAGAGGTGTAGTCTGCGGAAGGCGCAGATCACGTGCACAGTCA 502
QY	524 TCTTCTCTGTGATCGGGTGGCTGCTCTTTGTGCTCTCACTCTCACTCTTCTGTGTTCTCTACA 583
DB	503 TCTTTCATCTGTGTGGGGCGTCTTAGTCCACCTGGTGTATCCCAACCTTCGTATTCATGTGTA 562
QY	584 TGGAGAGCTGGACAGTATAGAGCCATCTACTTTGTTATAGTGACCTTCACCACTGTAG 643
DB	563 CTGAGGGGTGGAACTCATCGAGGGCTCTACTACTCTCTTCACTCACCATCTCCACCATCG 622
QY	644 GCTTTTCGCGATTATGTACCCGGCGATGGCACCGGGCAGAACTCTCCAGCC---TACCAGC 700
DB	623 GCTTCGGTGACTTGTGGCGGGTGTGAACCCAGCGCCAACCTACCAAGCCCTGTACCGCT 682
QY	701 CGCTGTGTGGTCTCGAATCTCTGTTGGCCCTAGCCTACTCTTGGCTCTAGTGTCTACCAACA 760
DB	683 ACTTCGTGAGCTCTGGATCTACTTGGGGCTGGCTGGCTGTCTCTCTTTTGTCACTCGA 742

QY 761 TCGGCAACTGGTTGCGGAGCAGT 782  
Db 743 AGGTGAGCATGTTTGTGGAAGT 764

RESULT 15

US-09-431-367B-1  
; Sequence 1, Application US/09431367B  
; Patent No. 6670149  
; GENERAL INFORMATION:  
; APPLICANT: Curtiss, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP  
; CURRENT APPLICATION NUMBER: US/09/431,367B  
; CURRENT FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 09/259,951  
; PRIOR FILING DATE: 1999-03-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3452  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10)..(1506)  
US-09-431-367B-1

Query Match 9.8%; Score 117.2; DB 4; Length 3452;  
Best Local Similarity 51.8%; Pred. No. 8.1e-23;  
Matches 384; Conservative 0; Mismatches 328; Indels 30; Gaps 4;  
QY 44 TTTACTTGGTATCTGGGGCTCTAGTGTTCAGGCTCTGGAGCAGCCTCACGAGCAGCAGG 103  
Db 50 TCTACTCTGGCCATCGGGGGCGCGCATCTTCGAGTCTGGAGGAGCCACACTGGAAGGAGG 109  
QY 104 CTCAGAGAAATGGATCATGCGCGAGCAGCAGTTCCTGAGGGACCATCCCTGTGTGAGCC 163  
Db 110 CCAAGAAACTACTACACAGAGAGCTGATCTGTCTCAAGGAGTTCCCGTGCCTGGGTC 169  
QY 164 AGAAGCCCTGGAGGATTTATCATAGCTCTCTGTTGAGCCCTGGAGGGGGCGAAACC 223  
Db 170 AGGAGGGCCTGGACAAGATCCTAGAGGTGGTATCTGATCTGAGGACAGGGGTGGGCCA 229  
QY 224 CAGAAACAGCTGGACCAATAGCAGCAACCACTCATCAGCTTGAACTGGCGAGCGCCT 283  
Db 230 TCACAGGGAACAGACCTTCAACAC-----TGGAACTGSCCAATGCAA 274  
QY 284 TCTTTTCTCGGGACCATCATACATCGGCTATGCAATATAGTCTTACACACAG 343  
Db 275 TGATTTTTCAGCGACCGCTCATACCACTTGGATATGCAATGCGCTCCCAAGACCC 334  
QY 344 ATGCGGGGCTCTTTTGTATCTTCTATGACTGGTGGGATCCCACTGTTCCGGATGC 403  
Db 335 CCGCCGGCTCGCCTTCTGTGTCTTCTATGCTCTTTCGGGGTGCCTCTGC----- 387  
QY 404 TGCTGGCGGAGTGGCGGACCGGCTCGCTCTCTCGCGCGGGGATCGGCCACATCG 463  
Db 388 ---CTGACGTGATCAGTGGCCCTGGGCAAGTCTTCGGGGGACGTGCCAAGAGAC---TAG 442  
QY 464 AAGCAATCTTTTGAAGTGGCATGTGCCACCGGGGCTGGTGAAGAGTCTGTCCGCAAGTGC 523  
Db 443 GGCAGTTCTTACCAAGAGAGGTGTGAGTCTGCGGAAGGCGCAGATCAGTGCACAGTCA 502  
QY 524 TCTTCTGCTGATCGGCTGCTCTTGTCTCTACCTCACTCTGCTGCTCTCTCTACA 583  
Db 503 TCTTCATCGTGTGGGGGCTCTAGTCCACTGGTGTCCCACTCCCTTCGTATTCATGTTGA 562  
QY 584 TGGAGAGCTGGAGCAAGTTAGAAGCCATCTACTTTTGTATAGTACTCTCACCACCTAG 643  
Db 563 CTGAGGGGTGGAATACATGAGGGGCTCTACTACTCTCTTCATCACCACCTCCACCATCG 622  
QY 644 GCTTTGGCGATTATGTATACCGGGGATGGCACCGGGGAGAACTCTCCAGCC---TACCAGC 700

Db 623 GCTTCGGTGACTTTGTGGCCGGTGTGAACCCAGCGCAACTACCAACGCTGTACCGCT 682  
QY 701 CGCTGGTGTGGTTCCTGGATCTTGTGGCTTAGCCTACTTGGCCTCAGTGTCTCACCACA 760  
Db 683 ACTTCGTGGAGCTCTGGATCTACTTGGGGCTGGCTGTCCCTTTTGTCAACTGGA 742  
QY 761 TCGGCAACTGGTTGCGAGCAGT 782  
Db 743 AGGTGAGCATGTTTGTGGAAGT 764

Search completed: February 2, 2005, 20:30:38  
Job time : 126 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	\$				
1	814.4	68.2	1182	14	US-10-243-035-1		Sequence 1, Appli
2	814.4	68.2	1257	9	US-09-828-035-3		Sequence 3, Appli
3	814.4	68.2	1257	15	US-10-146-733-30		Sequence 30, Appl
4	814.4	68.2	1260	15	US-10-345-680-45		Sequence 20, Appl
5	814.4	68.2	1260	15	US-10-391-399-20		Sequence 20, Appl
6	814.4	68.2	1408	9	US-09-828-035-1		Sequence 1, Appli
7	814.4	68.2	1408	15	US-10-146-733-28		Sequence 28, Appl
8	814.4	68.2	1408	15	US-10-352-584A-7		Sequence 7, Appli
9	814.4	68.2	1408	15	US-10-391-399-18		Sequence 18, Appl
10	814.4	68.2	2747	18	US-10-768-158-11		Sequence 11, Appl
11	814.4	68.2	2772	15	US-10-345-680-43		Sequence 43, Appl
12	811.4	68.0	3945	9	US-09-747-835A-30		Sequence 30, Appl





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Db 676 CTGAGGCCATCTACTTTGTATAGTGACCTTACCACCGTGGCTTTGGCGACTATGTG 735
Qy 661 CCGCGGATGGCAGCCGGGAGAACTCTCCAGCCTTACCAGCGCTGGTGTGTTCTGGATC 720
Db 736 GCGCGCGGAGACCCAGGAGGACTCCCGCGCTATCAGCGCTGTGTGTTCTGGATC 795
Qy 721 TTGTTTGGCTAGCTACTTTGGCTCAGTGTCTCACCACCATCGGCAACTGGTTGCGAGCA 780
Db 796 CTGCTCGGCTTGGCTTACTTTCGCTCAGTGTCTCACCACCATCGGCAACTGGCTGCGAGTA 855
Qy 781 GTGTCCCGCGAAGTCCGGGAGAGATGGGTGGCTTAAGGCAAGAGTGTCTAGCTGGACC 840
Db 856 GTGTCCCGCGCACTCCGGGAGAGATGGGTGGCTTACGGCTCAGGCTGCGAGTGGACT 915
Qy 841 GGCACAGTGAAGCGCGAGTGAAGCCAGCAAGTGGGCGGAGCGCGCGCGCGCGGAGAG 900
Db 916 GGCACAGTGAAGCGCGAGTGAAGCCAGCAAGTGGGCGGAGCGCGCGCGCGCGGAGAG 975
Qy 901 GAGCAACCACTCTGCGCTCTCTTTGCGGCGACCGCTGCTGTGTGTGAGCCAGCGGCG 960
Db 976 GAGCGCACTGC-----TGCTCCACCGCGCTGTCCAGCGCAGCGCTGGGC 1023
Qy 961 AGGCGCGCTCCCTGCACCGGAGAGAGTGTGAGACTTCGCTCCCGCGCGCGCGCTCA 1020
Db 1024 AGGCGCGGATCCCTTTCGCGCGCGGAGAGGCTCAGCGGCTTCCCGCGCGCGCGCTCG 1083
Qy 1021 GCTCTGATTTACCCAGTGAAGTCTGGCTTCTCATGACAGTCCCTCAGACGCGAGT 1080
Db 1084 GCGCTGATTTATCCACGAGAACTTGGCTTTCATGACAGTCTCTCGATACGAGAGC 1143
Qy 1081 GAGCGTGGCTGTGCGCTTCCCTCGGCTCTCTCGGCTCGCGCGCGCGCGCGCGCGCG 1140
Db 1144 GAGCGGCTGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203
Qy 1141 AAGCTTCCAGACCGCGGCTCTGGCGAGTCTCGGAGAGCGCGCTGCGCGGTG 1194
Db 1204 AAGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTG 1257

RESULT 4
US-10-345-680-45
; Sequence 45, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012P18NM OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
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; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1260)
US-10-345-680-45
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Query Match 68.2%; Score 814.4; DB 15; Length 1260;
Best Local Similarity 81.5%; Pred. No. 1.2e-233;
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;
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Qy 1 ATGCGGAGCACCACACTCTCTGGCTCTGCTGGGACACTGGTCTGCTTTTACTTTGGTATCTGGG 60
Db 79 ATGCGGAGCACCACACTCTCTGGCTCTGCTGGGACACTGGTCTGCTTTTACTTTGGTATCTGGT 138
Qy 61 GCTCTAGTGTTCAGGCTCTGAGGAGCTCTCAGCAGCAGGCTCAGAGAAATGGAT 120
Db 139 GCGCTGTGTTCGCGGCTCTGAGGAGCTCTCAGCAGCAGGCTCAGAGAAATGGAT 198
Qy 121 CATGGCCGAGACCACTTTCTGAGGAGCACTCTCTGCTGCTGAGCAGAGAGCTGGAGAT 180
Db 199 GAGGTCGAGAGAAAGTTCCTGAGGAGCACTCTGCTGCTGCTGAGGAGCTGGGCTC 258
Qy 181 TTCTATCAAGCTCTCTGTGTGAAGCTCTGGGAGGCGGCAAACTCCAGAAACCACTGGAC 240
Db 259 CTCATCAAGAGGTGCTGATGCTCTGGGAGGCGGCTGCGGACCCAGAAACCACTGGAC 318
Qy 241 AATAGCAGAAACCACTCTATCAGCTTGAAGCTCTGGGAGCGCTCTTTTCTGCGGGAGC 300
Db 319 AGCAACAGCAGGCTCTCTGAGGAGCTCTGAGGAGCTCTCTTTCTCAGGGAGC 375
Qy 301 ATCATCACTTACCATCGGCTATGCAATATAGTCTTACACACAGATGCGCGGCTCTCTTT 360
Db 376 ATCATCACCACCATCGGCTATGCAATATGCGGCTCTGCGCAGAGATGCGCGGCTCTTTC 435
Qy 361 TGTATCTTCTATGCACTGCTGGGAGTCCCACTGTTCGGGATGCTGCTGGGAGTCTGG 420
Db 436 TGCACTCTTATGCGCTGTGTGGGATTCGCTGTGTGGGATCTACTGCGAGGGTCTGG 495
Qy 421 GACCGCTGGGCTCTCTCTGCGCGGGGAGTGGGACATCGAGCAATCTCTTTGAAG 480
Db 496 GACCGCTGGGCTCTCTCTGCGGCTATGCGGCTGCGGCTGCGGCTGCGGCTCTCTTTGAAG 555
Qy 481 TGCGATGTGCGCACCGGCGCTGTGAGAGTCTGTCGCGAGTGTCTCTGCTGATCGGC 540
Db 556 TGCGAGTGTGCGCACCGGCGCTGTGAGAGTGTGTCGCGAGTGTCTCTGCTGATCGGC 615
Qy 541 TGCTGCTCTTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 616 TGCTGCTCTTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 675
Qy 601 TTAGAAGCCATCTACTTTGCTTATGAGTCTCTCAGCTCTCAGCTCTGAGCTTTGGCGAT 660
Db 676 CTGGAGGCACTACTTCTGCTATGAGTCTCTCAGCTCTCAGCTCTGAGCTTTGGCGAT 735
Qy 661 CCGCGGAGTGGCAGCCGCGGAGAACTCTCCAGCTCTCAGCTCTCAGCTCTGAGCTTTGG 720
Db 736 GCGCGGCGGAGCCCGGAGGAGTCTCCCGGCTATCAGCGCTGCTGCTGCTGCTGCTGCT 795
Qy 721 TTGTTTGGCTAGCTTACTTTGCTCTCAGTGTCTCAGCTCTCAGCTCTGAGCTTTGGCGAG 780
Db 796 CTGCTCGGCTTGGCTTACTTTGCTCTCAGTGTCTCAGCTCTCAGCTCTGAGCTTTGG 855
Qy 781 GTGTCCCGCGGAACTCGCGGAGAGTGGGTGGCTTAAGGCAAGAGTGTCTAGCTGGACC 840
Db 856 GTGTCCCGCGGCACTCGCGGAGAGTGGGTGGCTTACGGCTCAGGCTGCGAGTGGACT 915
Qy 841 GGCACAGTGAAGCGCGAGTGAAGCCAGCAAGTGGGCGGAGCGCGCGCGCGCGGAGAG 900
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1084	Db	GCCCTGATTATCCACGAGAACCTGGCTTATCAGCAGTCTCGGATACGCAGC	1143
1081	Qy	GAGCGTGGCTGTGCGCTCTCGGGCTCTCTCGGGTCCGCGCGACCAACCACTCCAA	1140
1144	Db	GAGCGCGGCTGCGCGTCTGCCCGCGCGCGAGAGGTGCGCGCGCCCAATCCCCCGG	1203
1141	Qy	AAGCCTTTCAGACCCCGGGGTCTCTGGCGCATCTCCGAGACAGGCCGTGCGCGTG	1194
1204	Db	AAGCCCGTGGCGCCCGCGCGCCCGCGCTCTCCCGAGACAAAGCGTGCCTGGT	1257

## RESULT 6

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US-09-828-035-1
; Sequence 1, Application US/09828035
; Patent No. US20020034781A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 12303, A NOVEL HUMAN TWIK MOLECULE AND USES THEREOF
; FILE REFERENCE: MNI-142
; CURRENT APPLICATION NUMBER: US/09/828,035
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 50/195,734
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84) .. (1340)
US-09-828-035-1

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Qy	541	TGCTGCTCTTTGTCCTCACTCTCACTTCCTGCTGTTCTCTCACTAGAGAGCTCGACGAAG	600
Db	699	TGCTGCTCTTTGTCCTCACTTCAGCCCACTGCTGCTTCTGCTATATGAGGAGCTCGACGAAG	758
Qy	601	TTAGAGCCATCTACTTTTGTATAGTGACTCTCACCACCTGTAGGCTTTGGCGATTATGTA	660
Db	759	CTGAGGCCATCTACTTTTGTATAGTGACGCTTACACCGTGGGCTTTGGCGACTATGTG	818
Qy	661	CCGGCGATGGCACCGGGCAGAACTCTCCAGCCTACACGCGCTGCTGTGGTTCCTGATC	720
Db	819	GCCGGCGGAGACCCAGGCAGGACTCCCGGCGCTATCAGCGCTGCTGTGTTCTGATC	878
Qy	721	TTGTTTGGCCTAGCTACTTTCGCTCAGTGCTCACCACCATCGGCAACTGGTTCGCGACA	780
Db	879	CTGCTCGGCTTGCTTACTTTCGCTCAGTGCTCACCACCATCGGAACTGGCTGCGAGTA	938
Qy	781	GTGTCCCGCGAACTCGGGCAGAGATGGGTGGGCTTAACGGCACAGGCTGTAGCTGGACC	840
Db	939	GTGTCCCGCGCACTCGGGCAGAGATGGGCGGCTCAGCGCTCAGGCTGCAGCTGGACT	998
Qy	841	GGCACAGTGACAGCGGAGTGACCCAGCGAACTGGGGCCAGCGCGCCCGCCAGAGAAAG	900
Db	999	GGCACAGTGACAGCGCGCTGACCCAGCGAGCGGGCGCCGCGCGCCCGCGCGGAGAAG	1058
Qy	901	GAGCAACACTCTGCCTCCTCTTTTGGCGGACCGGCTGCTGTGTTGAGCCAGCCGCGC	960
Db	1059	GAGCGACCATGC-----TGCTTCCACCGCCCTGTACGGCAGCGCTGGGC	1106
Qy	961	AGGCCCGGCTCCCTGTGACCCGCGAGAGAGTTGAGATCCGTCCTCCCGCCACGGGCTCA	1020
Db	1107	AGGCCCGATCCCTTGTCCGCCCGCGAGAGGCTCAGCGCTTCCCGCGCCACGGGCTCG	1166
Qy	1021	GCTCTGATTACCCCACTGAGAACTCTGGCCTTTCATCGACGAGTCTCTCAGACACGACAGT	1080
Db	1167	GCCCTGATTATCCACAGCGAGAACTGGCCCTTCATCGACGAGTCTCTCGGATACGACAGC	1226
Qy	1081	GAGGCTGGCTGTGCCCTGTCCGGCTCTCGGGGTCTCGCGGTCGCGCCGACCCCACTCCAAA	1140
Db	1227	GAGCGGGCTGCCGCTGTCCCGCGCGCAGAGGTGTCGCGCGCCCAATCCCCCAGG	1286
Qy	1141	AAGCCTTCCAGACCCCGGGGTCTCTGGGCGACTCCGAGACAAGGCGGTGCGGGT	1194
Db	1287	AAGTCCCTGCGGCTCCCGCGCTCCCGGCGCTCCCGGAGACAAAGCGGTGCGGGT	1340

## RESULT 7

US-10-146-733-28  
Sequence 28, Application US/10146733  
Publication No. US20030165891A1  
GENERAL INFORMATION:  
APPLICANT: Curtis, Rory A.J.  
APPLICANT: Glucksmann, Maria A.  
APPLICANT: Silos-Santiago, Immaculada  
TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,  
TITLE OF INVENTION: HNMDA-1, TWIK-9, alphazdelta-4, 54414, AND 53763 MOLECULES  
TITLE OF INVENTION: TITLE OF INVENTION: AND USES THEREFOR  
FILE REFERENCE: MNI-248  
CURRENT APPLICATION NUMBER: US/10/146,733  
CURRENT FILING DATE: 2002-05-15  
PRIOR APPLICATION NUMBER: US 60/185,938  
PRIOR FILING DATE: 2000-02-29  
PRIOR APPLICATION NUMBER: US 09/515,520  
PRIOR FILING DATE: 2000-02-29  
PRIOR APPLICATION NUMBER: US 09/518,866  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: US 60/195,734  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: US 60/195,993  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: US 60/199,799  
PRIOR FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: US 60/233,537



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; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)...(1343)
; US-10-352-684A-7

Query Match      68.2%; Score 814.4; DB 15; Length 1408;
Best Local Similarity 81.5%; Pred. No. 1.2e-233;
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;

QY      1  ATGCGAGCACACACTCTCTGGCTCTCTGGCACTGGTGTGCTTTACTTTGGTATCTGGG 60
DB      162 ATGCGAGCACACAGCTCTCTGGCCCTCTGGCGCTGGTGTGCTTTACTTTGGTGTCTGGT 221

QY      61  GCCTACTGTTCCAGGCTCTGGAGCAGCCTCACGAGCAGCAGGCTCAGAAAGAAAATGGAT 120
DB      222 GCCCTGTGTGTTCCGGGCCCTTGGACAGCCCCACGAGCAGCAGGCCAGAGGAGCTGGG 281

QY      121 CATGGCCGAGACCAAGTTTCTGAGGAGCATCTGTGTGAGCCAGAGAGCCTGGAGAT 180
DB      282 GAGTCCGAGAGAAAGTTCTCTGAGGGCCCATCCGTGTGTGAGCGCACGAGAGCTGGGCTC 341

QY      181 TTATCAAGCTCTCGTGTGAAGCCCTGGGAGGGGGCGCAACCCAGAAACCACTGGAC 240
DB      342 CTCAATCAAGGAGGTGGCTGATGGCCCTGGGAGGGGGTGGGACCCAGAAACCACTCGAC 401

QY      241 AATAGCAGCAACCACTCATACAGTTTGAACCTGGGCGAGCGCTTTCTTTTCTCGGGAGCC 300
DB      402 AGCAACAGCAGCCAC--TCAGCTTGGGACCTGGGCGAGCGCTTTCTTTTCTCAGGGAGCC 458

QY      301 ATCATCACTACCATCGGTATGGCAATATAGTCTTACACAGATCCCGGGGTCTCTTT 360
DB      459 ATCATCACCAACCATCGGCTATGGCAATATGGGCCCTGGCGACAGATGCCGGGCGCTCTTC 518

QY      361 TGTATCTTCTATGCACTGGTGGGATCCACTGTTTCGGGATGCTCTCTGGCGGAGTCTGG 420
DB      519 TGCATCTTTTATGCGCTCGTGGGGATTCGGCTGTTTGGGATCCCTACTTGCAGGGGTCTGG 578

QY      421 GACCGGCTGGGCTCTCTCTGCGCCGGGCGATCGGCCCATCGAAGCAATCTTCTTGAAG 480
DB      579 GACCGGCTGGGCTCTCTCTGCGCCCATGSGATCGGTCAATTGAAGCCATCTTCTTGAAG 638

QY      481 TGGCATGTGCAACCGGGGCTGTGAGAGTCTGTCCGAGTCTCTTCTCTGCTGATCGCG 540
DB      639 TGGCACGTGCCACCGGAGCTAGTAGAGTGTGTGGCGATGCTTTCTCTGCTGATCGCG 698

QY      541 TGCCGTGCTTTGTCTCTCACTCTCACTTCGTTGTTCTCTTACATGAGAGCTGGAGCAAG 600
DB      699 TGCCGTGCTTTGTCTCTACGCGCAGGTTCGTGTTCTGCTATATGAGGACTGGAGCAAG 758

QY      601 TTAGAAGCCATCACTTTGTTTATAGTGACTCTCAACACTGTAGGCTTGGCAATTATGTA 660

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; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)...(1343)
;
US-10-391-399-18
Query Match      68.2%; Score 814.4; DB 15; Length 1408;
Best Local Similarity 81.5%; Pred. No. 1.2e-233;
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;

QY 1 ATGCGAGACACACATCTCTGGCTCTGTGGCACTGGTGTCTTACTTGTGTCTGGG 60
DB 162 ATGCGAGACACACATCTCTGGCTCTGTGGCTCTGTGGCTCTGTGGCTCTGTGG 221
QY 61 GCTCTAGTGTCCAGCTCTGGAGCAGCTCTCAGCAGCAGCAGCTCAGAGAAATGGAT 120
DB 222 GCCTCTGGTGTCCGGGCTCTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 281
QY 121 CATGGCCGAGACACAGTTTCTGAGGACCACTCTCTGTGTGAGCAGAGAGCTGGAGGAT 180
DB 282 GAGGTCGAGAGAGTCTCTGAGGGCCATCTCTGTGTGAGCAGCAGAGCTGGGCTC 341
QY 181 TTCAATCAAGCTCTGTGTGAAGCCCTGGGAGGGGGCGCAAAACCCAGAACCTGAGC 240
DB 342 CTATCAAGAGGTGTCTGATGCTCTGGAGGGGGTGGGACCCAGAAACCACTCGAC 401
QY 241 AATAGCAGACACACTCATCAGTCTGGAACCTGGGAGCGCTCTTTTCTGGGAGC 300
DB 402 AGCAACAGCAGCCAC---TAGCCTGGGACCTGGGAGCGCTCTTTTCTCAGGAGC 458
QY 301 ATCATCACTACCATCGCTATGCAATATAGTCTTACACACAGATCGCGGCGCTCTTT 360
DB 459 ATCATCAACCACTCGCTATGCAATATGCGCTCTGGCCTGGGACAGATCGCGGCGCTCTTC 518
QY 361 TGTATCTTCTATGACTGTGGGATCCCACTGTTCGGGATGCTGTGGCGGAGTCGGG 420
DB 519 TGCATCTTTATGCGTGTGGGATTCGCTGTGTGGGATCTCTGCGCAGGGTCTGGG 578
QY 421 GACCGCTGGGCTCTCTCTGCGCGGGGATCGGCACATCGAAGCAATCTTTTGAAG 480
DB 579 GACCGCTGGGCTCTCTCTGCGCCATGCGCATCGGTACATTTGAAGCCATCTTTTGAAG 638
QY 481 TGGCATGTGCAACCGGGCTGTGAGAAGTCTCTCGCAGTGTCTTCTGCTGATCGGC 540
DB 639 TGGCAGTGGCACCGAGCTAGTAAGTGTCTGCGGATGCTTCTGCTGATCGGC 698
QY 541 TGCTGTCTTTGTCTCACTCTCTACCTCTGTTCTCTTCTACATGAGAGCTCGAGCAAG 600
DB 699 TGCTGTCTTTGTCTCACTCTCTACCTCTGTTCTCTTCTATATGAGAGCTGAGCAAG 758
QY 601 TTAGAAGCCATCTACTTTTATAGTACTCTACCACTGTAGCTTTGGCGATTATGTA 660
DB 759 CTGGAGGCCATCTACTTTGTATAGTACGCTTTACCACCGTGGCTTTGGCGACTATGTG 818
QY 661 CCCGGGATGGCACCGGCGAGAACTCTCCAGCCTTACCAGCGCTGTGTGTTCTGATC 720
DB 819 GCCGGCGCGAACCCAGCAGGACTCTCCCGGCTATCAGCCGCTGTGTGTTCTGATC 878
QY 721 TTGTTTGGCTAGCTACTTCTGCTCAGTGTCTACCAACCATCGCAACTGTGTTGCGAGCA 780
DB 879 CTGCTCGGCTGCTTACTTCTGCTCAGTGTCTACCAACCATCGGAACTGTGCTGCGAGTA 938
QY 781 GTGTCGCGCGAACTCTGGGAGAGATGGGTGGCTTAACGGCAGAGGCTGTAGCTGACC 840
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DB 939 GTGTCCCGCCACTCGGCGACAGATGGCGCCCTCACGGCTCAGGCTCCAGCTGGACT 998
QY 841 GGCACAGTACAGCGAGTGTAGCCAGCGAACTGGGCCAGCCGCCCGCCGCGAGAGAG 900
DB 999 GGCACAGTACAGCGCGCTGTAGCCAGCGAGCGCGGCCCGCCCGCGCGGAGAGAG 1058
QY 901 GAGCAACCACTCTCTGCTCTCTTTTGGCGGACCGCTCTGTTGTTGAGCCAGCGCGC 960
DB 1059 GAGCAGCCACTGC-----TGCCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 1106
QY 961 AGGCGCGGCTCCCTGTGACCCGCGAGAGAGTGTGAGCTCCGTCCCGCCGCGCGCTCA 1020
DB 1107 AGGCGCGGATCCCTTGTGCGCCCGGAGAGGCTCAGCGGCTTCCCGCGCGCGCTCG 1166
QY 1021 GCTCTGATTAACCCAGTGAATCTGGCTTCTATCGAGAGTCTCTACAGCAGCAGT 1080
DB 1167 GCCTTGGATTATCCAGCGAGAACCTTGGCTTTCATCGAGAGTCTCTCGATACGAGAGC 1226
QY 1081 GAGCGTGGTGTGCTCTGCTGCGCTCTCGGGTCTCGGGTCTCGCGGCGGACCAACCATCCAAA 1140
DB 1227 GAGCGCGGCTGCGCGCTGCTGCGCGCGCGAGAGTCTCGCGCGCGCCAAATCCCCCAGG 1286
QY 1141 AAGCTTTCAGACCCCGGGTCTCTGGCGACTCCGAGACAAAGCCCTGCGCGTG 1194
DB 1287 AAGCCGCTCGCGCCCGCGCGCGCTCCCGAGACAAAGGCTGCGCGTG 1340

RESULT 10
US-10-768-158-11
; Sequence 11, Application US/10768158
; Publication No. US20040204359A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliabof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 16386, 15402, 21165, 1423,
; TITLE OF INVENTION: 636, 12303, 21425, 27410, 38554, 38555, 57145, 59914,
; TITLE OF INVENTION: 94921, 16852, 33260, 58573, 30911, 85913, 14303, 16816,
; TITLE OF INVENTION: 17827 OR 32620
; FILE REFERENCE: MPI03-012PIRNONIM
; CURRENT APPLICATION NUMBER: US/10/768,158
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,781
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/452,291
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/454,540
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 60/478,805
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/491,048
; PRIOR FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2747
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)...(1310)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2747)
; OTHER INFORMATION: n = A,T,C or G
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US-10-768-158-11
Query Match      68.2%; Score 814.4; DB 18; Length 2747;
Best Local Similarity 81.5%; Pred. No. 1.5e-233;
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;
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1 ATGCGAGACCACTCTCTGGCTCTGTGGCACTGGTGTCTCTTACTTGGTATCTGGG 60  
129 ATGCGGACACACGCTCTCTGGCCCTGTCTGGCGCTGTCTTACTTGGTGTCTGGT 188  
61 GCTCTAGTGTTCAGGCTCTGAGAGCTCTGAGAGAGAGGCTCAGAGAAATGGAT 120  
189 GCCCTGGTGTTCGGGCGCTTGGAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAG 248  
121 CATGGCCGAGACCACTTCTGAGGAGACCATCTCTGTGAGCAGAGAGCTGGAGGAT 180  
249 GAGGTCGAGAGAGTCTCTGAGGCGCCATCTCTGTGTGAGCAGAGAGCTGGGCTC 308  
181 TTCTATCAAGCTCTCTGTGTTGAAGCCCTGGAGAGGCGCAAAACCGAGAACAGCTGGACC 240  
309 CTCTATCAAGGAGTGTCTGATCCCTTGGAGAGGAGTGGAGCCCAAGAACCACTCGACC 368  
241 AATAGAGAACCACTCATCAGCTTGGAGACCTGGGAGCGCTCTCTTCTTCTCGGGGACC 300  
369 AGCAACAGCAGCCAC---TCAGGCTGGGACCTGGGAGCGCTCTCTTCTCTCAGGAGCC 425  
301 ATCATCACTACCTCGGCTATGGCAATATAGTCTTACACAGATCCCGGGGCTCTCTTT 360  
426 ATCATCACTACCTCGGCTATGGCAATATAGTCTTACACAGATCCCGGGGCTCTCTTT 485  
361 TGTATCTTATGACCTGTGGGATCCCACTGTTCGGGATGCTGTGGGAGTGGG 420  
486 TGCATCTTTATGCGCTGTGGGATTCGCTGTTCGGGATGCTGTGGGAGTGGG 545  
421 GACCGCTGGGCTCTCTCTGCGCGGGGATCGGCAATCGGCAATCGGCAATCTCTTTGAAG 480  
546 GACCGCTGGGCTCTCTCTGCGCGGGGATCGGCAATCGGCAATCGGCAATCTCTTTGAAG 605  
481 TGGCATGTGCGACCGGGCTGTGAGAGTGTTCGCGAGTGTTCGCTGTCTGATCGGC 540  
606 TGGCAGTGTGCGACCGGAGTGTGAGAGTGTTCGCGAGTGTTCGCTGTCTGATCGGC 665  
541 TGCCTGTCTTGTGCTCTACCTCTACCTCTGCTGTCTCTACATGAGAGCTGGAGCAAG 600  
666 TGCCTGTCTTGTGCTCTACCTCTACCTCTGCTGTCTCTACATGAGAGCTGGAGCAAG 725  
601 TTGAGAGCATCTACTTTTGTATAGTACTCTACCACTGTAGGCTTTGGGATATGTA 660  
726 CTGAGAGCATCTACTTTGTATAGTACTCTACCACTGTAGGCTTTGGGATATGTA 785  
661 CCGCGGATGAGACCGGCGAGACTCTCCAGCTTACAGCGCTGTGTGTCTGTGATC 720  
786 GCGCGGCGGACCCCGAGGAGACTCTCCAGCTTACAGCGCTGTGTGTCTGTGATC 845  
721 TTGTTGGCTTAGCTACTTCTGCTCTAGTGTCTACCACTCTGGCAATCTGGAGCA 780  
846 CTGCTCGGCTGTCTTCTGCTCTAGTGTCTACCACTCTGGCAATCTGGAGTGA 905  
781 GTGTCGCGCACTCGGCGAGATGGTGGCTTAAGGACAGAGCTGTAGCTGGACC 840  
906 GTGTCGCGCACTCGGCGAGATGGGCGCTCTACAGCTGTAGCTGTAGCTGACT 965  
841 GGCACAGTGTGACGCGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 900  
966 GGCACAGTGTGACGCGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1025  
901 GAGCAACCACTCTCTGCTCTCTCTTGTGGGAGCGCTGTGTGTGAGGAGCGGCG 960  
1026 GAGCAGCACTG-----TGCCTTCCAGCGCTGTGTGAGGAGCGCTGTGGC 1073  
961 AGGCGCGCTCTCTGCAACCGGAGAGAGTGTGAGCTTCTGCTCTGCTCTGCTCTCA 1020  
1074 AGGCGCGCTCTCTGCAACCGGAGAGAGTGTGAGCTTCTGCTCTGCTCTGCTCTCA 1133  
1021 GCTCTGAGTATCCCGAGTGTGAGATCTGGCTCTCATCGAGTGTCTGAGAGCGAGT 1080  
1134 GCGCTGAGTATCCCGAGAGAGTGTGGCTCTCATCGAGTGTCTGAGTATCGAGAGC 1193  
1081 GAGGCTGGCTGTGCTCTCTCTGCGGCTCTCTGCGGCTCTCTGCGGAGCGCAACCACTCCAAA 1140

1194 GAGCGGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1253  
1141 AAGCCTTCAGAGCCCGGGGTCTGGGAGCTCCGAGAGCAAGGCGCTGCGCGGTG 1194  
1254 AAGCCGCTGCGGTG 1307  
RESULT 11  
US-10-345-680-43  
; Sequence 43, Application US/10345680  
; Publication No. US20030148394A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Venkateswarlu, Karicheti  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING 34021, 44099, 25278,  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 62553, 302, 323,  
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656,  
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MPI02-012P1RNM OMNI  
; CURRENT APPLICATION NUMBER: US/10/345,680  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/423,809  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/429,797  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 2772  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (64)....(1323)  
US-10-345-680-43  
Query Match 68.2%; Score 814.4; DB 15; Length 2772;  
Best Local Similarity 81.5%; Pred. No. 1.5e-233; Indels 15; Gaps 2;  
Matches 973; Conservative 0; Mismatches 206;  
1 ATGCGAGACCACTCTCTGGCTCTGTGGCACTGGTGTCTCTTACTTGGTATCTGGG 60  
142 ATGCGAGACACGCTCTCTGGCCCTGTCTGGCGCTGTCTTACTTGGTGTCTGGT 201  
61 GCTCTAGTGTTCAGGCTCTGAGAGCTCTGAGAGAGAGGCTCAGAGAAATGGAT 120  
202 GCCTGTGTTCGGGCGCTTGGAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAG 261  
121 CATGGCCGAGACCACTTCTGAGGAGACCATCTCTGTGTGAGCAGAGAGCTGGAGAT 180  
262 GAGGTCGAGAGAGTCTCTGAGGCGCCATCTCTGTGTGAGCAGAGCTGGGCTC 321  
181 TTCTATCAAGCTCTCTGTGTTGAAGCCCTGGAGAGGCGGCGCAAAACCGAGAACCACTCGACC 240  
322 CTCTATCAAGGAGTGTGCTGATGCTCTGCGGAGGCGGTGCGGAGCCCAACTCGACC 381  
241 AATAGCAGCAACCACTCATCAGCTTGGAACTCTGCGGAGCGCTTCTTTTCTCGGGAGCC 300









QY 901 GAGCAACACTCTCGCCCTCTCTTTCCGCGACCCGCTCTGTTGTGAGCCAGCCGCG 960  
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DB 2515 GAGCAGCACTGC-----TGCCCTCAACCGCCCTGTCAGCGCAGCCGCTGGCG 2562  
QY 961 AGGCCCGCTCCCTGTCACCGCAGAGAGGTTGAGACTCCGTCCTCCGCGCCACGGCTCA 1020  
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DB 2563 AGGCCCGATCCCTTCGCGCCCGAGAGAGCTCAGCGGCTTCCCGCGCCACGGCTCG 2622  
QY 1021 GCTCTGGATTACCCAGTGAAGTCTGGCTTTCATGACAGAGTCTCTCAGACAGCAGAGT 1080  
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DB 2623 GCCTGGATTATCCAGCAGAGAACCTGGCTTCTCATGACAGTCTCTCGGATACGAGAGC 2682  
QY 1081 GAGGTGGCTGTCCTGCTCCCTGCTGGCTCTCTGGGCTCGCGCGACCAAGCCATCCAAA 1140  
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DB 2683 GAGCGGGCTGCGCGCTGCGCGCGCGCGCGAGAGGTGCGCGCGCCCAAAATCCCGCCAGG 2742  
QY 1141 AAGCTTCCAGACCCCGGGGTCTGGGCGACTCCGAGACAAGCGCGCGCG 1191  
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DB 2743 AAGCCCGTGGCGCGCGCGCGCGCGCGCTCCCGAGACAAAGCGGTGCGG 2793

## RESULT 14

US-09-747-835A-28  
; Sequence 28 Application US/09747835A  
; Patent No. US20020146692A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE  
; FILE OF INVENTION: (Like) POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: HYS-37CIP  
; CURRENT APPLICATION NUMBER: US/09/747,835A  
; CURRENT FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: US 09/729,739  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: US 09/653,450  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US 09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US 09/598,042  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: US 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 3996  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (52)..(3996)  
US-09-747-835A-28

Query Match 68.0%; Score 811.4; DB 9; Length 3996;  
Best Local Similarity 81.4%; Pred. No. 1.3e-232;  
Matches 970; Conservative 0; Mismatches 206; Indels 15; Gaps 2;  
QY 1 ATGCGCAGCACCACTCTCGGCTCTGCTGGCACTGGTCTGCTTACTTGGTATCTGGG 60  
DB 1669 ATGCGCAGCACCACTCTCGGCTCTGCTGGCACTGGTCTGCTTACTTGGTCTGGT 1728  
QY 61 GCTCTAGTGTTCAGGCTCTGAGCAGCCTTCAGCAGCAGGCTCAGAGAAATGGAT 120  
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DB 1729 GCCTCGTGTTCGCGGCCCTTGAGCAGCCCAACAGCAGCAGAGGAGAGCTGGGG 1788  
QY 121 CATGGCCGAGACACAGTTTCTGAGGGACCAATCCCTCTGTGTGAGCAGAGACCTTGGAGAT 180  
DB 1789 GAGGTCCGAGAGAAGTTCTGTAGGGCCCATCCGTGTGTGAGCAGCAGAGGAGCTGGGCTC 1848  
QY 181 TTCTCAAGTCTCTGTGTTGAGGCCCTTGGAGGGGGGCGCAACCCAGAGAAACAGTGGACC 240  
DB 1849 CTCTCAAGGAGGTGGCTGATGCCCTTGGAGGGGGTGGGACCCAGAGAAACCAATCGACC 1908  
QY 241 AATAGCAGCAACCACTCATCAGCTTGGAACTCTGGCAGCGCCTTCTTTTCTGGGGACC 300  
DB 1909 AGCAACAGCAGCCAC---TCAGCTGGACCTGGCAGCGCCTTCTTTTCTCAGGACC 1965  
QY 301 ATCATCACTACCACTCGGCTATGCAATATAGTTTACACACAGATGCGCGGCTCTTTT 360  
DB 1966 ATCATCACCACTCGGCTATGCAATATGCGCCCTGCGCAGATGCGCGGCGCTCTTC 2025  
QY 361 TGTATCTTCTATGCACTGTGGGGATCCCACTGTTGGGATGCTGTGGGGGAGTGGG 420  
DB 2026 TGCATCTTTTATGCGCTGGTGGGGATTCGCTGTTTGGGATCTTACTGGCAGGGGTGG 2085  
QY 421 GACCGCTGGGCTCTCTCTGCGCCGGGCGCATCGGCACATCGAAGCAATCTTCTTGAAG 480  
DB 2086 GACCGCTGGGCTCTCTCTGCGCCATGGCATCGGTACATTTGAGGCATCTTCTTGAAG 2145  
QY 481 TGGCATGTGCCACCGGGGCTGTGAGAAGTCTGTCCGCACTGCTCTTCTGCTGATCGGC 540  
DB 2146 TGGCAGTGGCACCGGAGCTAGTAAGAGTGTCTGCGCGATGCTTTTCTGCTGATCGGC 2205  
QY 541 TGCCTGCTTGTGCTCTACTCTCTAGCTGTGCTTCTCTACATGAGAGCTGAGCAAG 600  
DB 2206 TGCCTGCTTGTGCTCTACTCTGCGCCACGCTTCTGCTATATGAGGAGCTGAGCAAG 2265  
QY 601 TTAGAGCCCATCTACTTGTGTAGTGACTCTCACCACCTGATGCTTGTGGCGATTATGTA 660  
DB 2266 CTGAGGCCATCTACTTGTGTATGATGACGCTTACACCGTGGCTTGTGGCATATGTG 2325  
QY 661 CCGCGGATGGCACCGGGCAGAACTCTCCAGCCTACACGCGCTGTGTGTGTTCTGATC 720  
DB 2326 GCGCGCGCGACCCAGGAGGACTCCCGGCTATCAGCGCTGTGTGTGTTCTGATC 2385  
QY 721 TTGTTTGGCTTAGCTTACTTTCGCTCAGTGTCTCACCACATCGGCACTGTTGTCGAGCA 780  
DB 2386 CTGCTCGGCTTGTCTTACTTTCGCTCAGTGTCTCACCACATCGGCACTGTTGTCGAGTA 2445  
QY 781 GTGTCGCGCGGAACTCGGCGAGATGGGTGGCTTAACGSCACAGGCTGTAGTGGACC 840  
DB 2446 GTGTCCCGCGCACTCGGCGAGATGGGCGGCTCAGGCTCAGGCTGCGAGTGA 2505  
QY 841 GGCACAGTGACAGCGGAGTGACCCAGCACTGGGCGCCAGCGCCCGCGCCAGAGAG 900  
DB 2506 GGCACAGTGACAGCGCGGTGACCCAGAGAGCGCGCGCGCGCGCGCGCGGAGAG 2565  
QY 901 GAGCAACCACTCTGCGCTCTCTTTGCGGGAACCGGCTGCTGTTGTTGAGCCAGCGCG 960  
DB 2566 GAGCAGCCACTGC-----TGCCCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 2613  
QY 961 AGGCCCGGCTCCCTTCACCGCAGAGAGGTTGAGACTCCGTCCTCCCGCCAGCGCTCA 1020  
DB 2614 AGGCCCGGATCCCTTTCGCGCCCGGAGAGGCTCAGCGGCTTCCCGCCAGCGGCTCG 2673  
QY 1021 GCTCTGGATTACCCAGTGAAGTCTGGCTTTCATGACAGAGTCTCTCAGACAGCAGAGT 1080  
DB 2674 GCGCTGATTATCCAGCGAGAACCTTGGCTTTCATGACAGAGTCTCTCGGATACGAGAGC 2733  
QY 1081 GAGGTGGTGTGCTGCTGCTGCGGCTCTCTGGGGTGGCGCGAGCCCAACCCATCCAAA 1140  
DB 2734 GAGCGGGGTGCGCGCTGCGCGCGCGGAGAGGTGCGCGCGCGCCCAATCCCGCCAGG 2793  
QY 1141 AAGCTTCCAGACCCCGGGGTCTTGGGCGACTCCGAGACAAAGCGCGCGCG 1191  
DB 2794 AAGCCGTGCGGCGCGCGCGCGCGCTCCCGAGACAAAGCGCGTGGCG 2844

## RESULT 15

US-10-037-270-195  
; Sequence 195, Application US/10037270  
; Publication No. US20030104529A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Tillinghast, John  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and  
; FILE OF INVENTION: Polyptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/10/037,270  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1104  
; SOFTWARE: PC\_FL\_genes Version 1.0  
; SEQ ID NO 195  
; LENGTH: 3996  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (52)..(3996)  
US-10-037-270-195

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Qy 61 GCTTAGTGTTCAGGCTCTGGAGCAGCTTCCAGCAGCAGGCTCAGAGAGAAATGAT 120  
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Db 1789 GAGTTCGAGAGAGATCTCTGGAGGACATCCCTGTGTGAGGAGCAGGAGCTGGGCTC 1848  
  
Qy 181 TTCAATCAAGCTCTCTGGTGAAGCCCTGGAGGGGGGCGCAACCCAGAGAAACAGCTGGACC 240  
Db 1849 CTCATCAAGGAGTGGCTGATGCCCTGGAGGGGGTGGGACCCAGAGAAACCACTCGACC 1908  
  
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Db 2086 GACCGGCTGGGCTCTCTCTGCGCCCATCGCATCGGTACATTTGAAGCCATCTTCTTGAAG 2145  
Qy 481 TGGCATGTGCCACCGGGGCTGGTGAAGAGTGTGTCCGAGTGTCTTCTGCTGTATCGGC 540  
Db 2146 TGGCAGTGTGCCACCGGAGCTAGTAAGAGTGTGTGCGGGATGCTTTTCTGCTGTATCGGC 2205  
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Qy 781 GTGTCCCGCGGAACCTCGGGCAGAGATGGGTGGCTTAAACGGCACAGGCTCTAGCTGGACC 840  
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Search completed: February 2, 2005, 22:13:15  
Job time : 734 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 16:25:10 ; Search time 4236 Seconds  
(without alignments)  
10271.256 Million cell updates/sec

Title: US-09-655-272-1\_COPY\_284\_1477

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Sequence: 1 atgcgcagaccacactct.....gagacaagccgtgcggtg 1194

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	540	45.2	581	6	CB606856 AMGNNUC:N
C 4	529.6	44.4	590	2	BE981482 UI-M-CGOp
C 5	517	43.3	593	2	BE981393 UI-M-CGOp
6	484.4	40.6	1560	3	CR603880 full-leng
7	420.2	35.2	469	2	BF565047 UI-R-BOL
8	419.4	35.1	1405	3	BC067791 Homo sapi
9	405.4	34.0	736	5	BX451513 BX451513
10	379.2	31.8	570	2	BB569111 BB569111
C 11	374.4	31.4	891	1	AL537214 AL537214
12	340.8	28.5	822	7	CK653558 AGENCOURT
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14	297.4	24.9	553	5	BM942654 UI-M-CGOp
15	284.8	23.9	498	5	BY248534 BY248534
C 16	284.4	23.8	627	7	CO039400 UI-M-BHO-
17	279.2	23.4	667	5	BU759620 UI-R-PFO-
18	259.4	21.7	613	9	AY405805 Pan trogl
19	259.4	21.7	1745	3	AK036066 Mus muscu
20	259.4	21.7	2534	3	AK082153 Mus muscu
21	257.2	21.5	406	6	CB808226 AMGNNUC:S
22	254.8	21.3	2628	3	AK031904 Mus muscu
23	241.4	20.2	448	5	BY252956 BY252956
24	229.2	19.2	1113	9	AY418067 Mus muscu

25	224.2	18.8	1129	4	BM544559	BM544559	AGENCOURT
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27	205.6	17.2	772	6	CB959623	CB959623	AGENCOURT
28	204.8	17.0	413	5	BY283120	BY283120	BY283120
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C 33	173.2	14.5	698	8	BZ201163	BZ201163	CH230-303
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35	171.2	14.3	920	5	BQ948206	BQ948206	AGENCOURT
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C 37	153.6	12.9	462	2	AW527208	AW527208	UI-R-BOL-
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43	143.2	12.0	885	9	AY404469	AY404469	Homo sapi
44	135.6	11.4	879	9	AY404471	AY404471	Mus muscu
45	133.2	11.2	775	7	CN528767	CN528767	UI-M-HQ0-

#### ALIGNMENTS

RESULT 1	AY405806	1197 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	Mus musculus KCNK4 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY405806				
VERSION	AY405806.1	GI:39761780			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 1197)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1197)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
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ORIGIN					
Query Match	100.0%;	Score 1194;	DB 9;	Length 1197;	
Best Local Similarity	100.0%;	Pred. No. 5.6e-299;			
Matches 1194;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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DEFINITION genomic survey sequence.  
ACCESSION AY405804  
VERSION AY405804.1 GI:39761778  
KEYWORDS GSS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1182)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1182)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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Best Local Similarity 81.5%; Pred. No. 2.4e-200;  
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;  
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DB 1 ATGCGCAGCACCACTCTCTGCTCTGCTGGCACTGGTCTCTTACTTGGTATCTGGT 60  
QY 61 GCTCTAGTGTTCAGGCTCTGAGCAGCCTCTCAGCAGCAGGCTCAGAGAAATGGAT 120  
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VERSION CB606856.1 GI:29546469
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ORGANISM Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 581)
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AUTHORS  
TITLE  
JOURNAL  
COMMENT

Angen EST Program.  
Angen Rat EST Program  
Unpublished (2003)  
Contact: Dan Fitzpatrick  
Angen, Inc  
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
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Location/Qualifiers

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Best Local Similarity 95.7%; Pred. No. 4.1e-129;  
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Qy 663 CCGCGATGCGACCGGGGAGAACTCTCCAGCTTACAGCGGCTGGTGTGGTCTGATCTT 722  
Db 482 AGGCGATGCGACCGGGGAGAACTCTCCAGCTTACAGCGGCTGGTGTGGTCTGATCTT 541  
Qy 723 GTTGGCTTAGCTACTTTCGCTCAGTGTCTACCACTATC 762  
Db 542 GTTGGCTTAGCTACTTTCGCTCAGTGTCTACCACTATC 581

RESULT 4  
BE981482/c  
LOCUS

DEFINITION UI-M-CGop-bdc-f-10-0-UI-s1 NIH BMAP Ret4 S2 Mus musculus cDNA clone  
ACCESSION BE981482  
VERSION BE981482.1 GI:10650633  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 590)

AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mEST@mail.nih.gov  
Oligo-dt track not found, Not 1 site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine  
Seq primer: M13 Forward  
POLYA=No.

FEATURES  
source  
1..590  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-CG0p-bdb-f-10-0-UI"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NIH BMAP Ret4 S2"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NIH BMAP Ret4 S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine  
TAG\_SEQ=None found"

ORIGIN  
Query Match 44.4%; Score 529.6; DB 2; Length 590;  
Best Local Similarity 99.3%; Pred. No. 2.1e-126; Indels 0; Gaps 0;  
Matches 532; Conservative 0; Mismatches 4;

QY 1 ATCGGAGCACCACACTCTGGCTCTGCTGGCACTGGTCTGCTTTACTTGTATCTGGG 60

DB 551 ATCGGAGCACCACACTCTGGCTCTGCTGGCACTGGTCTGCTTTACTTGTATCTGGG 492

QY 61 GCTCTAGTGTCCAGGCTCTGGAGAGGCTCTAGAGCAGGCTCAGAGCAAGCAATGGAT 120

DB 491 GCTCTAGTGTCCAGGCTCTGGAGAGGCTCTAGAGCAGGCTCAGAGCAAGCAATGGAT 432

QY 121 CATGGCCGACACAGTTCTGAGGGACCACTCTGCTGTGAGCCAGAGCAAGCAATGGAT 180

DB 431 CATGGCCGACACAGTTCTGAGGGACCACTCTGCTGTGAGCCAGAGCAAGCAATGGAT 372

QY 181 TTCAATCAAGCTCTCTGGTGAAGCCCTGGAGGGGGGGGCAAAACCCAGAACAGCTGGACC 240

DB 371 TTCAATCAAGCTCTCTGGTGAAGCCCTGGAGGGGGGGGCAAAACCCAGAACAGCTGGACC 312

QY 241 AATGAGCAGCACCACTCATGCTTGGAACTCTGGGAGCGCCCTCTTTTCTCGGGGACC 300

DB 311 AATGAGCAGCACCACTCATGCTTGGAACTCTGGGAGCGCCCTCTTTTCTCGGGGACC 252

QY 301 ATCATCACTACCATCGGCTATGCGCAATATAGTCTTACACAGATGCGGGCGTCTCTTT 360

DB 251 ATCATCACTACCATCGGCTATGCGCAATATAGTCTTACACAGATGCGGGCGTCTCTTT 192

QY 361 TGTATCTTCTATGCACTGCTGGGATCCCACTGTTGGGATGCTCTGCTGGGATGCGGG 420

DB 191 TGTATCTTCTATGCACTGCTGGGATCCCACTGTTGGGATGCTCTGCTGGGATGCGGG 132

QY 421 GACCGGCTGGGCTCTCTCTGCGCGGGCATCGGCACATCGAAGCAATCTTCTTGAAG 480

DB 131 GACCGGCTGGGCTCTCTCTGCGCGGGCATCGGCACATCGAAGCAATCTTCTTGAAG 72

QY 481 TGGCATGTGCCACCGGGGCTGGTGAAGTCTCTGCGAGTCTCTCTCTGCTGAT 536

DB 71 TGGCATGTGCCACCGGGGCTGGTGAAGTCTCTGCGAGTCTCTCTCTCAAGAAGAT 16

RESULT 5

BE981393 593 bp mRNA linear EST 29-APR-2002

LOCUS UI-M-CG0p-bdb-f-11-0-UI.s1 NIH BMAP Ret4 S2 Mus musculus cDNA clone

DEFINITION UI-M-CG0p-bdb-f-11-0-UI 3', mRNA sequence.

ACCESSION BE981393

VERSION BE981393.1 GI:10650455

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 593)

AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mEST@mail.nih.gov  
Oligo-dt track not found, Not 1 site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine  
Seq primer: M13 Forward  
POLYA=No.

FEATURES  
source  
1..593  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-CG0p-bdb-f-11-0-UI"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NIH BMAP Ret4 S2"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NIH BMAP Ret4 S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine  
Seq primer: M13 Forward  
POLYA=No.

ORIGIN	TAG_SEQ=None found"	division of Invitrogen. Location/Qualifiers 1. .1560 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DF019YL24" /tissue_type="fetal brain" /plasmid="PCWVSPORT_6"	FEATURES source	ORIGIN
Query Match Best Local Similarity Matches 528; Conservative	43.3%; Score 517; DB 2; Length 593; 99.8%; Pred. No. 3.9e-123; 0; Mismatches 0; Indels 1; Gaps 1;	40.6%; Score 484.4; DB 3; Length 1560; 80.4%; Pred. No. 1.4e-114; 0; Mismatches 131; Indels 12; Gaps 1;		
Qy	1 ATGGCGAGCACCACACTCTCTGGCTCTGCTGGCACTGTGTGCTGTCTTACTTTGATCTCTGGG 60	467 CAATCTTCTTGAAGTGGCATGTGCCACCGGGGTGTGTGAGAACTGTCTGTCCGCACTGTCT 526		
Db	554 ATGGCGAGCACCACACTCTCTGGCTCTGCTGGCACTGTGTGCTGTCTTACTTTGATCTCTGGG 495	595 CCATCCCGCAGAGTGGCAGCTGCCACCGGAGCTAGTAGAGTGTCTCGCGCATGCTTT 654		
Qy	61 GCTCTAGTGTCCAGGCTCTGGAGCAGCTTCCAGCAGCAGCAGCTCAGAGAAATGGAT 120	527 TCCTGTGATCGGCTGCTGTCTTTGTCTCTACTCTCTACTCTTCTGCTGTCTTCTCTACATGG 586		
Db	494 GCTCTAGTGTTCAGGCTCTGGAGCAGCTTCCAGCAGCAGCAGCTCAGAGAAATGGAT 435	655 TCCTGTGATCGGCTGCTGTCTTTGTCTCTCAACGCCACGTTCTGCTGTCTGTCTATATGG 714		
Qy	121 CATGGCGGAGACCACTTCTGAGGGACCATCTCTGTGTGAGCAGAGAGCCTCGAGGAT 180	587 AGAGCTGGAGCAGATTAGAGCCATCTACTTGTGTATAGTACTCTCACCACCTGAGGCT 646		
Db	434 CATGGCGGAGACCACTTCTGAGGACCATCTCTGTGTGAGCAGAGAGCCTCGAGGAT 375	715 AGAGCTGGAGCAGATTAGAGCCATCTACTTGTGTATAGTACTCTCACCACCTGAGGCT 774		
Qy	181 TTCAATCAAGCTCTCTGGTTGAAGCCCTGGAGGGGGGCAAAACCCAGAAACACAGCTGAGCC 240	647 TTGGCCATTATGTATCCCGCGATGGCAGCCGGGAGAACTCTCCAGGCTTACACGCGCTGG 706		
Db	374 TTCAATCAAGCTCTCTGGTTGAAGCCCTGGAGGGGGGCAAAACCCAGAAACACAGCTGAGCC 315	775 TTGGCCATTATGTATCCCGCGATGGCAGCCGGGAGAACTCTCCAGGCTTACACGCGCTGG 834		
Qy	241 AATAGCAGCAACCACTCATCAGCTTGGAACTTGGAACTTGGAACTTGGAACTTGGAACTTGGAA 300	707 TGTGTTCTTGGATCTTTGTTGGCTAGCTTACTTTCGCTCTAGTGTCTACCAATCTGGCA 766		
Db	314 AATAGCAGCAACCACTCATCAGCTTGGAACTTGGAACTTGGAACTTGGAACTTGGAACTTGGAA 255	835 TGTGTTCTTGGATCTTTGTTGGCTAGCTTACTTTCGCTCTAGTGTCTACCAATCTGGCA 894		
Qy	301 ATCATCACTACCTATGCAATATATAGTCTTACACAGATGCGGGGCTCTCTTT 360	767 ACTGTTGGAGCAGTGTCCCGGCACTCGGGCAGAGATGGGTGGCTTAAACGCGCAGG 826		
Db	254 ATCATCACTACCTATGCAATATATAGTCTTACACAGATGCGGGGCTCTCTTT 195	895 ACTGTTGGAGCAGTGTCCCGGCACTCGGGCAGAGATGGGTGGCTTAAACGCGCAGG 954		
Qy	361 TGTATCTTCTATGACTGTGGGATCCCACTGTTCGGGATGTCTGTCGGGAGTCGGG 420	827 CTGCTAGCTGGACCGGCACTGACAGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 886		
Db	194 TGTATCTTCTATGACTGTGGGATCCCACTGTTCGGGATGTCTGTCGGGAGTCGGG 135	955 CTGCTAGCTGGACCGGCACTGACAGCGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1014		
Qy	421 GACGGCTGGGCTCTCTGCGCGGGGATCGGCACATCGGCACATCGAAGCAATCTTTGAG 480	887 CGCCGCCAGAGAGAGCAACCACTCTGCTCTCTCTTTCGCGCAGCAGGCTGTGCTTTG 946		
Db	134 GACGGCTGGGCTCTCTGCGCGGGGATCGGCACATCGGCACATCGAAGCAATCTTTGAG 75	1015 CGCCGCCAGAGAGAGCAACCACTCTGCTCTCTCTTTCGCGCAGCAGGCTGTGCTTTG 1062		
Qy	481 TGGCATGTGCGCAGCGGGCTGTGTGAGAGTCTGT-CCGAGTGTCTTTC 528	947 TTGAGCAGCGCGCAGCGCGGCTCCCTGCAACCGCAGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 1006		
Db	74 TGGCATGTGCGCAGCGGGCTGTGTGAGAGTCTGTCCCGCAGTGTCTTTC 26	1063 CGCAGCGCTGTGGCAGCGCGGCTCCCTGCGCGCGCGGAGAGGCTTACGCGGCTTTC 1122		
RESULT 6				
CR603880				
LOCUS	1560 bp mRNA linear HTC 21-JUL-2004			
DEFINITION	full-length cDNA clone CS0DF019YL24 of Fetal brain of Homo sapiens (human).			
ACCESSION	CR603880			
VERSION	CR603880.1 GI:50484687			
KEYWORDS	HTC; CNSLT cDNA.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope. 2 (bases 1 to 1560)			
REFERENCE				
AUTHORS				
TITLE	Direct Submission			
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segret@genoscope.cns.fr)			
COMMENT	- Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the PCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a			
BP565047	469 bp mRNA linear EST 12-DEC-2000			
LOCUS	UI-R-B01-ajm-g-02-0-UI.r1 UI-R-B01 Rattus norvegicus cDNA clone			
DEFINITION	UI-R-B01-ajm-g-02-0-UI 5', mRNA sequence.			



Clone distribution: MGC clone distribution information can be found  
here: <https://image.llnl.gov>

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15718766  
This clone has the following problem: retained intron.

## FEATURES

source  
1. 1405  
/location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30345701"  
/tissue\_type="Placenta, normal"  
/clone\_lib="NIH MGC\_147"  
/lab\_host="DH10B"  
/note="vector: pBluescript"

## ORIGIN

Query Match 35.1%; Score 419.4; DB 3; Length 1405;  
Best Local Similarity 69.6%; Pred. No. 1.1e-97;  
Matches 697; Conservative 0; Mismatches 141; Indels 163; Gaps 3;  
QY 194 TGGTTGAAGCCCTGGGAGGGGGCGGCAAAACCCAGAAACCACTGGACCAATAGCAGCAACC 253  
DB 247 TGGCTGATGCTGGGAGGGGGTGGGACCCAGAAACCACTGGACCAACAGCAGGCC 306  
QY 254 ACTCATCAGCTTGGAACTGGGAGCGCTCTTTTCTCGGGACCATCATCACTACCA 313  
DB 307 AC---TCAGCTGGGACCTGGGAGCGGCTCTTTTCTCAGGAGCCATCATCACCACCA 363  
QY 314 TCGGCTATGGCAATATAGTCTTACACAGATGCGGGGCTCTTTTGTATCTTCTATG 373  
DB 364 TCGGCTATGGCAATATGCTGGGCTGGGACAGATGCGGGGCTCTTCTGATCTTTATG 423  
QY 374 CACTGTGGGATCCCACTGTTCCGGATGCTGTGGCGGAGTGGGGACCGCTGGCT 433  
DB 424 CGCTGTGGGATTCGCTGTTTGGGATCTTCTGCGAGGGTGGGGACCGGCTGGCT 483  
QY 434 CTTCTGCGCGGGGATCGGACACATCGAAGCAATCTTCTGAAGTGCATGTGCCAC 493  
DB 484 CTTCTGCGCGGATGGCATCGGTACATGAAGCCATCTTCTT-----526  
QY 494 CGGGGCTGGTGAAGTCTGTCGCGAGTCTTCTCTGCTGATCGGCTGCTGCTCTTTG 553  
DB 527 -----526  
QY 554 TCCTCACTCTACTCTTGGTGTCTCTTACATGAGAGCTGGAGCAAGTTAGAGCCATCT 613  
DB 527 -----526  
QY 614 ACTTTGTATAGTCACTCTCACCACCTGTAGGCTTTGGCGATTATGTACCCGGCGATGGCA 673  
DB 527 -----GTGACGCTTACCACCGTGGGCTTTGGCGACTATGTGGCGGCGCGGACC 575  
QY 674 CCGGGCAGAACTCTCCAGCCTACAGCGCTGTGTGTGTTCTCGATCTTGTGTTGGCTAG 733  
DB 576 CAGGAGAGGACTCCCGGCTATACGCGCTGTGTGTGTTCTGATCTCTGCTCGGCTGG 635  
QY 734 CTTACTTGGCTCAGTGTCTCACCACCATCGGAACTGGCTGCGAGTAGTGTCTCCCGCGCA 695  
DB 636 CTTACTTGGCTCAGTGTCTCACCACCATCGGAACTGGCTGCGAGTAGTGTCTCCCGCGCA 695  
QY 794 CTGGGAGAGATGGTGGCTTAACGGCACAGGCTGTAGCTGGACCGGCACAGTACAG 853  
DB 696 CTGGGAGAGATGGGCGGCTCACGGCTCAGGCTGCGAGTGGGACAGTACAG 755  
QY 854 CGGAGTACCCAGCAACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 913  
DB 756 CGGCGTACCCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 815  
QY 914 TGCCCTCTCTTTTCCGGCACCGCGCTGCTGTGTGTGAGCCAGCGGCGGCGGCGGCTCCC 973  
DB 816 -----TGCTTCCACCGGCTGTCCAGCGAGCGGCTGGGCGGCGGCGGCGGCGGCGGCTCC 863  
QY 974 CTGACCCGAGAGAGTGTGAGATCTCGTCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1033

DB 864 CTTTGGCCCCCGAGAGGCTCAGCCGCTTCCCGCGGCGGCTCGGCCCTGGATATATC 923  
QY 1034 CCAGTGAGAACTTGGCTTTCATCGACGAGTCTCTCAGACACGACGAGTGGCTGTG 1093  
DB 924 CCAGCGAGAACTTGGCTTTCATCGACGAGTCTCTCGATAGCGACGAGCGGCTGCC 983  
QY 1094 CCTGCTCGGCTCTCTCGGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1153  
DB 984 CGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1043  
QY 1154 CCGGGGCTCTCTGGGCGACTCCGAGACAGCGCGTGGCGGTG 1194  
DB 1044 CCGCGGCGGCGGCGGCGGCTCCCGGAGACAAAGGCGTGGCGGTG 1084

## RESULT 9

EX451513  
LOCUS  
DEFINITION  
EX451513 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
CS0DF019YL24 5-PRIME, mRNA sequence.

## ACCESSION

EX451513

## VERSION

EX451513.2

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 736)

## AUTHORS

Li, W. B., Gruber, C., Jessee, J., and Polaves, D.

## TITLE

Full-length cDNA libraries and normalization

## JOURNAL

Unpublished (2001)

## COMMENT

On May 22, 2003 this sequence version replaced gi:31026267.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 6303.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?se=CS0BAF015ZF10\_AF01423\_l&c=6303.f

## FEATURES

## source

1. 736

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DF019YL24"

/tissue\_type="FETAL BRAIN"

/dev\_stage="fetal"

/clone\_lib="Homo sapiens FETAL BRAIN"

/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

## ORIGIN

Query Match 34.0%; Score 405.4; DB 5; Length 736;  
Best Local Similarity 80.3%; Pred. No. 4.1e-94;  
Matches 505; Conservative 0; Mismatches 111; Indels 13; Gaps 2;  
QY 566 CTTTCTGTTCTCTACATGGAGCTGGAGCGAGTAGAGCCATCTACTTTTATAG 625  
DB 7 CGTTCTGTTCTGCT-TATGGAGCACTGGAGCAAGCTGGAGGCCATCTACTTTGTCTAG 65  
QY 626 TGAATCTCACCCTGTAGGCTTTGGCGATTATGTACCCGCGGATGGCACCGGCGAGACT 685  
DB 66 TGACGCTTACCCTGGGCTTTGGCGACTATGTGTGCGCGGCGGACCCGAGGAGACT 125





/issue type="testis, pooled"  
/lab host="NIH MGC 237"  
/notes="Organ: testis; Vector: pExpress-1; Site 1: EcorV;  
Site 2: NotI; RNA obtained from testis tissue of 8 wk old  
animal. Tissues were snap-frozen and kept at -80C before  
RNA extraction and purification (Tri-reagent method). cDNA  
was primed using oligo-dT primer:  
5'-pGACTAGTCTAGATCGAGCGGCCGCTT-3' and cloned into  
the EcorV/NotI sites of pExpress-1. Size-selection >1.4kb  
resulted in an average insert size of 2.4 kb. This primary  
library is not normalized (normalized primary library is  
NIH MGC 238) and was constructed by Express Genomics  
(Frederick, MD)"

ORIGIN

Query Match 28.5%; Score 340.8; DB 7; Length 822;  
Best Local Similarity 93.6%; Pred. No. 2.6e-77;  
Matches 367; Conservative 0; Mismatches 22; Indels 3; Gaps 1;  
803 AGATGGGTGGCTTAACGGCAAGCTGTCTAGCTGGACCGGCAAGTGCAGCGCGAGTGA 862  
141 AGATGGGTGGCTTACGGCGCAGGCTGTCTAGCTGGACCGGCAAGTGCAGCGAGTGA 200  
863 CCCAGCGAATCTGGCCCGCAGCGCCCGCGCCGAGAGGAGCAACACTCTCTCCCTCTT 922  
201 CCCAGAGAACTGGACCCAGCGCCCGCGCCGAGAGGAGCAACACTCTCTCCCTCTT 260  
923 CTTTGGCGGCAACCGCTGTCTGTGTGAGCGAGCGCGCCGCGCTCCCTGCAACCG 982  
261 CTTTGGCGGCAACCGCTGTCTGTGTGAGCGAGCGCGCCGCGCTCCCTGCAACCG 320  
983 CAGAGAGGTTGAGACTCTGCTCCCGCGCCGCGCTGTCTGTGATACCCAGTGA 1042  
321 CAGAGAGGTTGAGACTCTGCTCCCGCGCCGCGCTGTCTGTGATACCCAGTGA 377  
1043 ATCTGGCGCTTCATGACGAGTCTCTCAGACGCGAGAGTGGCTGTGCTGCTC 1102  
378 ATCTGGCGCTTCATGACGAGTCTCTCAGACGCGAGAGTGGCTGTGCTGCTC 437  
1103 GGGCTCTCTGGGGTCCGCGCGCAACCAACCATTCAGAGCTTCAGAGCGCGGGTC 1162  
438 GTGCGCTCTGGGGTCCGCGCGCCCAACCAACCATTCAGAGCTTCAGAGCGCGGGTC 497  
1163 CTGGCGGACTCGAGACAGCGCGTGGCGGTG 1194  
498 CTGGCGGACTTCGAGACAGCGCGTGGCGGTG 529

RESULT 13

BI758226 922 bp mRNA linear EST 25-SEP-2001  
LOCUS 603029871F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5200313 5',  
DEFINITION mRNA sequence.  
ACCESSION BI758226  
VERSION BI758226.1 GI:15749804  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 922)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-f@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: L1AM1501 row: m column: 18  
High quality sequence stop: 785.  
FEATURES  
Location/Qualifiers  
1..922  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5200313"  
/lab host="DH108"  
/clone lib="NIH\_MGC\_114"  
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: EcorV (destroyed); RNA source anonymous pool of 6  
male brains, age range 23-27 yo. Library is oligo-dT  
primed and directionally cloned (EcorV site is destroyed  
upon cloning). Average insert size 1.5 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH\_MGC Library."

ORIGIN

Query Match 26.7%; Score 318.8; DB 4; Length 922;  
Best Local Similarity 82.0%; Pred. No. 1.4e-71;  
Matches 392; Conservative 0; Mismatches 82; Indels 4; Gaps 2;  
QY 1 ATGCGCAGCACAC-ACCTCTGGCTCTGTGCACTGGTGTCTTACTTGGTATCTGG 59  
DB 134 ATGCGCAGCACACTGCTCTCTGGCCCTGTGCTCTTGTCTTACTTGGTGTCTGG 193  
QY 60 GGCTCTAGTGTTCAGGCTCTGGAGCAGCTCAGCAGCAGCAGCTCAGAGAAATGGA 119  
DB 194 TGCCCTGTGTTCGGGCGCTTGGAGCAGCCCAAGCAGCAGCAGCAGGAGGAGTGG 253  
QY 120 TCATGCGCAGACCACTTCTGTGAGGACCATCCCTGTGTGAGCCAGAGAGCCTGGAG 179  
DB 254 GGAGGTCCGAGAGAGTCTCTGAGGCGCCATCCGTGTGTGAGCGACCAAGAGCTGGCG 313  
QY 180 TTTCTATCAAGTCTCTGGTTGAAGCCCTGGAGGGGGCCCAACCCAGAGAAACAGCTGGAC 239  
DB 314 CCTCATCAAGGAGGTGGCTGATGCTCTGGAGGGGGTGGAGCCCAAGAGAAACCACTCGAC 373  
QY 240 CAATAGCAACCACTCATCATGCTTGGAAACCTGGGAGCGCTTCTTTTCTCGGGGAC 299  
DB 374 CAGCAACAGCAGCCAC---TCAGCCTGGGACCTGGGAGCGGCTCTCTTTCTCAGGGAC 430  
QY 300 CATCATCACTACATCGGCTATGGCAATATAGTCTTACACACAGATGCCGGCGCTCTTT 359  
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DB 491 CTGCATCTTTTATGCCCTGTGGGATTCGCTGTTTGGATCCTTACTTGGCAGGGGTCTGG 550  
QY 420 GGAACCGCTGGGCTCTCTCTGCGCGGGGCAATCGGCCCATCGAGAGCAATCTTTTG 477  
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RESULT 14

BM942654 553 bp mRNA linear EST 29-APR-2002  
LOCUS BM942654  
DEFINITION UI-M-CGOp-bdb-f-11-0-UI.r1 NIH\_BMAP Ret4\_S2 Mus musculus cDNA clone  
ACCESSION UI-M-CGOp-bdb-f-11-0-UI 5', mRNA sequence.  
VERSION BM942654  
KEYWORDS EST.  
SOURCE BM942654.1 GI:19402517  
ORGANISM Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 553)  
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.

**TITLE** Normalization and subtraction: two approaches to facilitate gene discovery

**JOURNAL** Genome Res. 6 (9), 791-806 (1996)

**MEDLINE** 97044477

**PUBMED** 889548

**COMMENT** Contact: Chin, H  
National Institute of Mental Health  
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20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: meste@mail.nih.gov  
Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of Medicine  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
Seq primer: M13 REVERSE.

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**ORIGIN**  
Query Match 24.9%; Score 297.4; DB 5; Length 553;  
Best Local Similarity 96.5%; Pred. No. 4.4e-66;  
Matches 304; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 241 AATAGCAGCAACCACTCATCAGCTTGAAACCTGGGAGCGCCCTCTTTTCTCGGGGACC 300  
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QY 301 ATCATCACTACCATC 315  
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**RESULT 15**  
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LOCUS BY248534 RIKEN full-length enriched, visual cortex Mus musculus  
DEFINITION

**ACCESSION**  
BY248534  
**VERSION**  
BY248534.1  
**KEYWORDS**  
EST.  
**SOURCE**  
Mus musculus (house mouse)

**ORGANISM**

**REFERENCE**  
AUTHORS

CDNA clone K230317009 5', mRNA sequence.

BY248534

GI:26430046

EST.

Mus musculus (house mouse)

Mus musculus

1 (bases 1 to 498)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osaoto, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perteau, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, W., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
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Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute

Thu Feb 3 07:31:01 2005

RIKEN 2-1 Hiroawa,Wako-shi,Saitama 351-0198 Japan ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES  
source  
1. .498  
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Matches 289; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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201 ATGGCGAGCACCACACTCCCTGGCTCTGCTGGCACTGGTGTCTTTACTTGGTATCTGGG 260  
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321 CATGCCGAGACGAGTTCTGAGGGACCATCCCTGTGTGAGCCAGAGAGCCTGGAGGAT 380  
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381 TTCATCAAGCTCCTGGTTGAAGCCTGGAGGGGGCGCAACCCAGAAACCAAGTGGACC 440  
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QY	141	AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys	160
DB	704	GACCGCTGGCTCTCTCTCGCGCGGGCATCGGCACATCGAGCAATCTTCTGAAG	763
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DB	884	TTAGAGCAATCTACTTTGTATAGTGACTCTCACCACTGTAGGCTTGGCGATTATGTA	943
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DB	1184	GAGCAACCACTCTGCTGCTCTCTTGTGCGGACCGCTCTGTTGTGTAGCCAGCGGC	1243
QY	321	ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer	340
DB	1244	AGGCCCGGCTCCCTGCACCGCAGAGAAGTTGAGACTCCGTCGCCGCCACGGCTCA	1303
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DB	1304	GCTCTGGATTACCCAGTGAGAACTTGGCTTCTATCGAGAGTCTTCAGACGACAGT	1363
QY	361	GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys	380
DB	1364	GAGCGTGGCTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1423
QY	381	LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal	398
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LOCUS			
DEFINITION	Mus musculus TRAAK K+ channel subunit mRNA, complete cds.		
ACCESSION	AF056492		
VERSION	AF056492.1 GI:3329456		
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SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 1795)		
AUTHORS	Fink, M., Lesage, F., Duprat, F., Heurteaux, C., Reyes, R., Fosset, M. and Lazdunski, M.		
TITLE	A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids		
JOURNAL	EMBO J. 17 (12), 3297-3308 (1998)		
MEDLINE	98292450		
PUBMED	9628867		
REFERENCE	2 (bases 1 to 1795)		
AUTHORS	Fink, M., Lesage, F., Duprat, F., Heurteaux, C., Reyes, R., Fosset, M. and Lazdunski, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-APR-1998) Institut de Pharmacologie Molculaire et Cellulaire, CNRS UPR 411, 660 route des Lucioles, Valbonne 06560, France		
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Score:	2079.00	Matches:	398

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-655-272-2 (1-398) x AF056492 (1-1795)			
QY	1	MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuTyriLeuValSerGly	20
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QY	21	AlaLeuValPheGlnAlaLeuGlnProHisGlnGlnAlaGlnLysLysMetAsp	40
DB	344	GCTCTAGTGTCCAGGCTCTGGAGCCTCTCAGCAGCAGGCTCAGAGAAATGGAT	403
QY	41	HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp	60
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DB	644	TGTATCTTCTATGCTGCTGGGATCCCATGTTCTGGGATGCTGCTGGCGAGTCTGGG	703
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QY	201	LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal	220
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QY	221	ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValPheTyrIle	240
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DB	1004	TTGTTTGGCTAGGCTACTCTCCCTCAGTCTCACCACATCGCAACTGTTTGGAGCA	1063
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DB	1364	GAGCGTGGCTGTGCTCTGCTCGGCTCTCTCGGGTCTCGCGGACCAACCCATCCAAA	1423
QY	381	LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal	398
DB	1424	AAGCCTTCCAGACCCCGGGTCTCTGGCGACTCCGAGCAAGGCCGCTGCCGGTG	1477
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DEFINITION	mRNA, complete cds.		
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VERSION	AF302842.2	GI:17981766	
KEYWORDS	Rattus norvegicus (Norway rat)		
SOURCE	Rattus norvegicus		
ORGANISM	Rattus norvegicus		
REFERENCE	1 (bases 1 to 1194)		
AUTHORS	Kim, Y., Bang, H., Gnatenco, C. and Kim, D.		
TITLE	Synergistic interaction and the role of C-terminus in the activation of TRAAK K <sup>+</sup> channels by pressure, free fatty acids and alkali		
JOURNAL	Pfluegers Arch. 442 (1), 64-72 (2001)		
MEDLINE	21268449		
PubMed	11374070		
REFERENCE	2 (bases 1 to 1194)		
AUTHORS	Kim, Y. and Kim, D.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-SEP-2000) Physiology, Finch University of Health Sciences/The Chicago Medical School, 3333 Green Bay Road, North Chicago, IL 60064, USA		
REFERENCE	3 (bases 1 to 1194)		
AUTHORS	Kim, Y. and Kim, D.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-DEC-2001) Physiology, Finch University of Health Sciences/The Chicago Medical School, 3333 Green Bay Road, North Chicago, IL 60064, USA		
REMARK	Sequence update by submitter		
COMMENT	On Dec 27, 2001 this sequence version replaced gi:14334013.		
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CDS			
ORIGIN			
Alignment Scores:	4.88e-79	Length:	1194
Pred. No.:			

Score: 1975.50 Matches: 377  
Percent Similarity: 96.98% Conservative: 9  
Best Local Similarity: 94.72% Mismatches: 11  
Query Match: 95.02% Indels: 1  
DB: 1 Gaps: 1

US-09-655-272-2 (1-398) x AF302842 (1-1194)

QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuValSerGly 20  
DB 1 ATGGCAGCACCACACTCTCTGGCTCTGTCGCACTGGTGTCTTACTTTGGTATCTGGG 60  
QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGlnGlnAlaGlnLysLysMetAsp 40  
DB 61 GCTCTGGTGTATGCTCTGGAGCAGCTCATGAGCAGCAGTTTCTGAGGAGCCTGGAA 120  
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
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QY 61 PheileLysLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
DB 181 TTCTCATCAAGCTCTGGTGAAGCCCTGGGAGGGGGGCAACCCAGAAACCACTGGACC 240  
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
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QY 141 AspArgLeuGlySerSerLeuArgArgGlyileGlyHisileGluAlaIlePheLeuLys 160  
DB 421 GACCGGCTGGGCTCTCTCTGCGCGGGGCGATCGGTACATCGAAGCAGTTTCTTGAAG 480  
QY 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuileGly 180  
DB 481 TGGCATGTGCCACAGGCTGGTGAGAACTCTGCTGCGGTGCTCTTCTGTTGATTTGGC 540  
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrrMetGluSerTrpSerLys 200  
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QY 201 LeuGluAlaIleTyrrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrrVal 220  
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QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrrGlnProLeuValTrpPheTrpIle 240  
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DEFINITION Sequence 1 from patent US 6426197.  
ACCESSION AR221261  
VERSION AR221261.1 GI:23328170  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 1182)  
TITLES Duckworth, D.M. and Chapman, C.G.  
JOURNAL Polynucleotides encoding a human potassium channel  
Patent: US 6426197-A 1 30-JUL-2002;  
FEATURES Location/Qualifiers  
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Pred. No.: 1,45e-66 Length: 1182  
Score: 1692.50 Matches: 328  
Percent Similarity: 88.44% Conservative: 24  
Best Local Similarity: 82.41% Mismatches: 41  
Query Match: 81.41% Indels: 5  
DB: 6 Gaps: 2

US-09-655-272-2 (1-398) x AR221261 (1-1182)

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QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
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QY 121 CysilePheTyrrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
DB 358 TGCATCTTTATGCGCTGGTGGGATTCGCTGTTTGGGATCTCTACTTGGCAGGGGTGGGG 417

141 AsArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
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161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180  
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RESULT 6  
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ACCESSION AX250709  
VERSION AX250709.1 GI:15984447  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Lazdunski, M., Lesage, F. and Maingret, F.  
TITLE Novel family of mechanically sensitive human potassium channels  
JOURNAL activated by polyunsaturated fatty acids and use thereof  
Patent: WO 0168670-A 1 20-SEP-2001;  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)  
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Pred. No.: 1,45e-66 Length: 1182  
Score: 1692.50 Matches: 328  
Percent Similarity: 88.44% Conservative: 24  
Best Local Similarity: 82.41% Mismatches: 41  
Query Match: 81.41% Indels: 5  
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DB 61 GGCCTGTGTTCGGGCGCTTGGAGCAGCCGCCAGCAGCAGCAGCCAGAGGAGTGGGG 120  
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
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QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
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QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
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ORIGIN
Alignment Scores:
Pred. No.: 1,73e-66 Length: 1408
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: Gaps: 2

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DB 222 GCCTGTGTGTTCGGGCGCTTGGAGCAGCCACAGCAGCAGCAGCAGGAGGTGGG 281
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DB 282 GAGGTCCGACAGAGTTCCTGAGGGCCCATCGGTGTGAGCAGCAGGAGCTGGGCTC 341
QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerThr 80
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QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
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QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
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QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 579 GACGGCTGGGCTCTCTCCCTGGCCGATGGATGGTACATTCAGCCATCTTCTTGAAG 638
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
DB 639 TGGCAGCTGTCACCGGAGCTAGTAAGAGTGTCTGGCGGATGCTTTTCTGCTGATCGGC 698
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DB 759 CTGAGGCCCATCTCTTTGTCTAGTGACGCTTACCACTGGGCTTGGCGACTATGTG 818
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
DB 819 GCCGGCGGACCCAGCAGGAGCTCCCGGCGCTATCAGCGCTGGTGTGTTCTGGATC 878
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Db	1306 AGGCCCCGATCCCTTCCGCCCGCAGAGGCTCAGCGCTTCCCGCCGACGAGCTCG 1365	
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VERSION		Homo sapiens (human)
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REFERENCE		1 (bases 1 to 1730)
AUTHORS		Ozaita,A. and Vega-Saenz de Miera,E.
TITLE		Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human two-pore K+ channel gene KCN4. Chromosomal localization, tissue distribution and functional expression
JOURNAL		Brain Res. Mol. Brain Res. 102 (1-2), 18-27 (2002)
REFERENCE		2 (bases 1 to 1730)
AUTHORS		Ozaita,A. and Vega-Saenz de Miera,E.C.
TITLE		Direct Submission
JOURNAL		Submitted (21-APR-2000) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA
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QY	361	GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgGlyArgProAsnProSerLys	380
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Db	1367	AAGCCCGTGGCG	1420
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DEFINITION	Homo sapiens two pore K+ channel KT4.1b mRNA, complete cds.		
ACCESSION	AF259501		
VERSION	AF259501.1	GI:13925517	
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1	(bases 1 to 2747)	
AUTHORS	Ozaita, A. and Vega-Saenz de Miera, E.		
TITLE	Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human two-pore K+ channel gene KCN4. Chromosomal localization, tissue distribution and functional expression		
JOURNAL	Brain Res. Mol. Brain Res. 102 (1-2), 18-27 (2002)		
REFERENCE	2	(bases 1 to 2747)	
AUTHORS	Ozaita, A. and Vega-Saenz de Miera, E.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-APR-2000) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA		
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QY	61	PheIleLeuLeuValGluAlaLeuGlyGlyGlyAlaAanProGluThrSerTyrThr	80
Db	422	CTCATCAGGAGTGGCTGATCCCTCGGAGGGGTGGGACCCAGAACCACTCGACC	481
QY	81	AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr	100
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ACCESSION AF247042  
VERSION AF247042.1 GI:7576934  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Gray, A.T.  
TITLE Assignment of KCNK4 encoding the human potassium channel TRAAK to  
chromosome 11  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2772)  
AUTHORS Gray, A.T.  
TITLE Direct Submission  
JOURNAL Submitted (21-MAR-2000) Anesthesia, Room S 261, UC San Francisco,  
513 Parnassus Avenue, San Francisco, CA 94143-0542, USA

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gene  
CDS

Alignment Scores:  
Pred. No.: 3 41e-66 Length: 2772  
Score: 1692.50 Matches: 328  
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Best Local Similarity: 82.41% Mismatches: 41  
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ACCESSION AR338704
VERSION AR338704.1 GI:33725561
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3996)
AUTHORS Tang, Y.T., Zhou, P. and Drmanac, R.T.
TITLE Nucleic acids and polypeptides
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US-09-655-272-2 (1-398) x AR338704 (1-3996)

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Rachupka, A., Ranasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (01-OCT-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jul 26, 2003 this sequence version replaced gi:31880200.  
 All repeats were identified using RepeatMasker:  
 Smit, A.P.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WfBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence.submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L26033  
 Center clone name: 493\_E\_6  
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## Alignment Scores:

Pred. No.: 8,16e-54 Length: 181489  
 Score: 1453.00 Matches: 335  
 Percent Similarity: 41.55% Conservative: 2  
 Best Local Similarity: 41.31% Mismatches: 0  
 Query Match: 69.89% Indels: 474  
 DB: 10 Gaps: 4

US-09-655-272-2 (1-398) x AC120557 (1-181489)

QY 62 IleLysLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThrAsn 81  
 Db 82922 CTGCAGCTCTGGTTGAAGCCCTGGGGGGGCGCAACCCAGAAACCACTGGACCAAT 82981  
 QY 82 SerSerAsnHisSerSerAlaTrpAsnLeuGlyGlySerAlaPhePheSerGlyThrIle 101  
 Db 82982 AGCAGCAACCACTCATCAGCTTGGAAACCTGGGCGGCGCTCTTTTCTCGGGACCATC 83041  
 QY 102 IleThrThrIle----- 105  
 Db 83042 ATCACTACCATCGTGGGGTGGAGACGGGCGCATGTGGAGGAGCGAGGGCAAGGAGT 83101  
 QY 105 ----- 105  
 Db 83102 TTCCCTGTGGGGAAGGTGCAGGGAGAGCGAGGGGTACCCAGGTGGCACTTAGAATTTCT 83161  
 QY 106 -----GlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLe 119  
 Db 83162 GCAGTCCCTCTCCATCCAGGCTATGGCAATATAGTCTTACACACAGATCCCGGGGTCT 83221  
 QY 119 uPheCysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuAlaGlyVa 139  
 Db 83222 CTTTGTATCTTCTATGCATGCTGGGGATCCCACTGTTCCGGAATGCTGCTGGGGAGT 83281  
 QY 139 lGlyAspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLe 159  
 Db 83282 CGGGACCGGCTGGGCTCCTCTCTGCGCGGGGCATCGGCCACATCGAAGCAATCTTCTT 83341  
 QY 159 u----- 159  
 Db 83342 GGTGAGCTGCACTGCACCCCTCACAGGGTCTTCTTCCCTAGGTCCCTGGCAAGTAGTGT 83401  
 QY 159 ----- 159  
 Db 83402 GCCTCTCTAGAGAGAGGAGCCCTCTCACACACTATGCCAGATGGGGGTAGGGGGGTG 83461  
 QY 159 ----- 159

Db	83462	AGAGGGGTGAGAGAAATGGAATTGTTAGTCTTACTGGCATCTCAATGGCTCTATCTCCACCC	83521	Db	84542	TTTGTAAAGCAGACAGAAATCAGGAGGATTGCTGCGAGTTTAGACTTGGCTGGGTTATAGA	84601
Qy	160	-----LysTrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPh	176	Qy	268	-----	268
Db	83522	TTCCCCACAGAAAGTGGCATGTGCCACCGGGGCTGGTGAAGTCTGTCCGAGTCTCTT	83581	Db	84602	ATGAGACTCTGTTTCAAAAAACAACAGAACTAGAAAGCCAGTTATATGTGAATTCAGAT	84661
Qy	176	eLeuLeuIleGlyCysLeuLeuPheValLeuThrProThrPheValPheSerTrpMetG1	196	Qy	268	-----	268
Db	83582	CTTGCTGATCGGCTGCTCTTGTCTCACTCTACCTCTCGTGTCTCTCTACATGGA	83641	Db	84662	GAACACGAATACGATTTTAAGCTATGTGCCAAATATTGCATGAGTCGTCCTGGTTTGT	84721
Qy	196	uSerTrpSerLysLeuGluAlaIleTrpPheValIleValThrLeuThrValGlyPh	216	Qy	268	-----	268
Db	83642	GAGCTGGAGCAAGTTAGAGCCATCTACTTGTGTATAGTACTCTCACCACGTAGGCTT	83701	Db	84722	AAATTAATCTGCATTTTGTAGTCCAAATATACAGAGGCGAGTGAAGTTGAAAAACCCGA	84781
Qy	216	eGlyAspTrpValPro-----	221	Qy	268	-----	268
Db	83702	TGGCGATTATGTACCCGGTGAGTCTGCCCTTGGCCAGCATTAAGTACTTTGTTCCTGCAC	83761	Db	84782	GGCTTTCAGAAAGGTTCTTAGAGAGGGAGTGCTTTTGGGCCAAATGCAGGAAGGCACAG	84841
Qy	221	-----	221	Qy	268	-----	268
Db	83762	TCCGCCTATGCATCTACTGTGGGGCATTTGGCCAGCTTCCACACCAATCCTGGAAACCA	83821	Db	84842	TGTGGCTCTGGGATCATCCACAGGCTGAGGTTCAAGGTCAGGCAAAAAAGGTGGATGCAA	84901
Qy	221	-----	221	Qy	269	-----M	269
Db	83822	TACTTTCTTAGCAGGAGCCCTGTAGTCCACTTACATCTTGCATGCTGAGTCCCAT	83881	Db	84902	TTGGTAAAGGGCAGCTTTTCGGAGCTGCAATGGGTGCAACCCCTTTCTCTCTGTGCAGA	84961
Qy	221	-----	221	Qy	269	etGlyGlyLeuThrAlaGlnAlaIleSerTrpThrGlyThrValThrAlaArgValThrG	289
Db	83882	GCCTGCTCACACATATATTAAAGTTACCCCTCTTGATGCTCTTATACAGTTTACGACTG	83941	Db	84962	TGGGTGGCTTAACGGCACAGGCTGCTAGTGGACCGGCACAGTACAGCGCGAGTGACCC	85021
Qy	221	-----	221	Qy	289	InArgThrGlyProSerAlaProProGluLysGluGlnProLeuLeuProSerSerL	309
Db	83942	GAGTACTCATTTGTATACATCTACACATTATACACATCCCTTCTTTCTAGGAGGG	84001	Db	85022	AGCGAACTGGGCGCCAGCGCCCGCCGAGAGAGGACCAACCACTCTCTGCCCTCCTCTT	85081
Qy	221	-----	221	Qy	309	euProAlaProProAlaValValGluProAlaGlyArgProGlySerProAlaProAlaG	329
Db	84002	AGTGTCTTAAAGTGCAGAAACAGGAGTGGTCCAGAGGCTCACAGGCTTGCCTCCCC	84061	Db	85082	TGCCGGCACCGCTGCTGTTGTTGAGCCAGCCGCGCGGCTCCCTGCACCCCGCAG	85141
Qy	222	-----GlyAspGlyThrGlyG1	227	Qy	329	luLysValGluThrProSerProProThrAlaSerAlaLeuAspTrpProSerGluAsnL	349
Db	84062	CCACCCCCCATCACTTACTTTTCCCTCCCTTTGAACCGCTAGGCGATGGCACCGGGCA	84121	Db	85142	AGAAAGTTGAGACTCCGTCGCCGCCACCGGCTCAGCTCTGATTTACCCCGAGTGAATC	85201
Qy	227	nAsnSerProAlaTrpGlnProLeuValTrpPheTrpIleLeuPheGlyLeuAlaTrpPh	247	Qy	349	euAlaPheIleAspGluSerSerAspThrGlnSerGluArgGlyCysAlaLeuProArgA	369
Db	84122	GAACCTCTCAGCCTACCAAGCCGCTGGTGTGGATCTTGTGGCTTAGCTACTT	84181	Db	85202	TGGCTTTTCAATCCAGCATCTCTCAGACACGAGTGGCTGTGCCCTGCCTCGGG	85261
Qy	247	eAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArgArgThrArgAl	267	Qy	369	laProArgGlyArgArgProAsnProSerLysLysProSerArgProArgGlyProG	389
Db	84182	CGCTCAGTGTCTACCCATCGCACTGGTTGGAGCAGTGTCCCGCCGAACCTCGGGC	84241	Db	85262	CTCCTCGGGGTGCGCGCCGACCAACCCATCCAAAAAGCCTTCCAGACCCCGGGGTCTTG	85321
Qy	267	aGlu-----	268	Qy	389	lyArgLeuArgAspLysAlaValProVal	398
Db	84242	AGAGGTAATTTTACGTGTTCCAGAGTGTTCGCTGCGCGCATCGGCCATGCATGCTC	84301	Db	85322	GGCGACTCCGAGACAAGGCGGTGCCGGTG	85350
Qy	268	-----	268	Db			
Db	84302	TTGTGTGTGCTTATCCCGGGCACAGGGTGTGTGGCCAGTCTGTGCTCCCTTCCAAA	84361				
Qy	268	-----	268				
Db	84362	ATGTGGGCTTCTCTGACATTGAGACCCGAGCGGTGCGTTAACGGGAAACATTGGAGTAAT	84421				
Qy	268	-----	268				
Db	84422	TCAGGTTTGTACAGACTCAACCACTCGTTCTTCTGTGATAGATAGGCTGTACGGGTT	84481				
Qy	268	-----	268				
Db	84482	AGCAATAAGAACTCAGAGAGGCAAGTGTGTAGGTAGTACTGTCTGTAAATCCCGAGCAC	84541				
Qy	268	-----	268				

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 20:13:51 ; Search time 609.438 Seconds  
(without alignments)  
3428.193 Million cell updates/sec

Title: US-09-655-272-2

Perfect score: 2079

Sequence: 1 MRSTTLALLLVLYVSG.....SKKSPRPGRLRDKAVPV 398

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US09655272/runat\_02022005\_141714\_6735/app\_query.fasta\_1.1102  
-DB=N\_Geneseq\_23Sep04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09655272 @CIGN 1.1 586 @runat\_02022005\_141714\_6735 -NCPUs=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq\_23Sep04.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2079	100.0	1794	2 AAZ10606	Aaz10606 cDNA enco
2	1692.5	81.4	1182	3 AAA27105	Aaa27105 Human h-t
3	1692.5	81.4	1182	4 AAH78636	Aah78636 Human mec
4	1692.5	81.4	1218	3 AAA27106	Aaa27106 Human h-t
5	1692.5	81.4	1257	6 AAH99922	Aah99922 Nucleotid
6	1692.5	81.4	1257	12 AD127937	Ad127937 Human TWI

7	1692.5	81.4	1260	12 ADH51640	Adh51640 Human 123
8	1692.5	81.4	1408	6 AAH99921	Aah99921 Nucleotid
9	1692.5	81.4	1408	10 ADK52549	Adk52549 Hematolog
10	1692.5	81.4	1408	12 ADH51638	Adh51638 Human 123
11	1692.5	81.4	1408	12 ADI27935	Adi27935 Human TWI
12	1692.5	81.4	2772	10 AAD58498	Aad58498 Human pot
13	1692.5	81.4	2772	12 ADP21365	Adp21365 Gene KCNK
14	1688.5	81.2	3945	8 ABX91950	Abx91950 Human G p
15	1688.5	81.2	3996	5 AAS08652	Aas08652 Human cDN
16	1688.5	81.2	3996	5 ADQ98525	Adq98525 DNA encod
17	1688.5	81.2	3996	6 ABX91949	Abx91949 Human G p
18	1688.5	81.2	3996	9 ADB48285	Adb48285 Novel hum
19	1683.5	81.0	3945	5 AAS11984	Aas11984 Human cDN
20	1554.5	74.8	1337	4 AAH78646	Aah78646 Human mec
21	895	43.0	1265	4 ABA09473	Aba09473 Human K c
22	812	39.1	1614	6 AAI27558	Aai27558 ORF of hu
23	812	39.1	1614	6 AAD27459	Aad27459 Human TWI
24	812	39.1	1632	6 AAD34451	Aad34451 Human TRE
25	812	39.1	1632	6 ABK27503	Abk27503 DNA encod
26	812	39.1	1644	6 ABN85879	Abn85879 Hypothala
27	812	39.1	1870	10 ADE07404	Ade07404 Novel cod
28	812	39.1	2028	8 ADA05745	Ada05745 Human NOV
29	812	39.1	2028	12 ADN62309	Adn62309 Human NOV
30	812	39.1	2065	6 ABK49585	Abk49585 Human cDN
31	812	39.1	2730	6 ABZ11550	Abz11550 Human pol
32	812	39.1	2730	12 ADM44068	Adm44068 Novel hum
33	784	37.7	1994	2 AAZ00040	Aaz00040 Mouse h-t
34	784	37.7	3580	3 AAD17497	Aad17497 Murine TR
35	778	37.4	1236	3 AAD17496	Aad17496 Human TRE
36	778	37.4	1246	2 AAZ00039	Aaz00039 h-TREK1 p
37	778	37.4	1246	2 AAC90412	Aac90412 Human TRE
38	778	37.4	1993	2 AAZ10607	Aaz10607 cDNA enco
39	778	37.4	2391	11 ADP03564	Adp03564 Human GPC
40	778	37.4	3300	2 AAZ11915	Aaz11915 Human pot
41	775.5	37.3	2820	6 AAL44676	Aal44676 Human tra
42	761	36.6	2130	4 AAS12169	Aas12169 Human pot
43	757	36.4	2130	4 AAS12181	Aas12181 Human pot
44	756	36.4	2130	4 AAS12182	Aas12182 Human pot
45	755	36.3	2130	4 AAS12183	Aas12183 Human pot

#### ALIGNMENTS

RESULT 1  
AAZ10606  
ID AAZ10606 standard; cDNA; 1794 BP.  
XX  
AC AAZ10606;  
XX  
DT 18-NOV-1999 (first entry)  
XX  
DE AAZ10606  
XX  
DE AAZ10606  
XX  
KW Mechanically sensitive potassium channel protein; TPAAK;  
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;  
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
KW muscular disease; ds.  
XX  
OS Mus sp.  
XX  
FH Key  
CDS Location/Qualifiers  
FT FT 284..1480  
FT /\*tag= a

PN WO9945108-A2.

XX

PD 10-SEP-1999.

XX

PF 23-FEB-1999; 99WO-FR000404.

XX

PR 05-MAR-1998; 98FR-00002725.

XX



XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Chapman CG, Duckworth DM;  
 XX WPI; 2000-365583/31.  
 DR P-PSDB; AAY94425.  
 XX Novel isolated h-TRAAK polypeptides belonging to the potassium channel  
 PT family of polypeptides, useful for the diagnosis and treatment of h-TRAAK  
 PT related disorders, e.g. depression and schizophrenia.  
 XX Claim 5; Page 21; 35pp; English.  
 XX Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK  
 CC polynucleotides from human tissue samples. h-TRAAK polypeptides have  
 CC homology to the 2p domain potassium channel family of polypeptides. The h  
 CC -TRAAK polypeptides and polynucleotides may be used in diagnostic assays  
 CC for conditions related to h-TRAAK imbalance and for identifying agonists  
 CC and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and  
 CC polynucleotides may also be useful for treatment and prevention (e.g. as  
 CC vaccines) of certain diseases, such as pain, psychiatric disorders  
 CC including depression and schizophrenia, neurodegenerative disease  
 CC including Alzheimer's, stroke and head trauma and neurological disorders  
 CC including migraine and epilepsy. The present sequence is human h-TRAAK-1  
 CC cDNA sequence #1  
 XX SQ Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3,44e-84 Length: 1182  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 88.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5  
 Gaps: 2

US-09-655-272-2 (1-398) x AAA27105 (1-1182)

QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuValLeuValSerGly 20  
 DB 1 ATCCGACGACACACGCTCTCTGGCCCTGCTGGCGCTGCTTGTCTTACTTGTGTCTGT 60  
 QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysMetAsp 40  
 DB 61 GCCCTGTGTCTCCGGGCGCTGGAGCAGCCACAGCAGCAGCAGCAGCAGGAGCTGGGG 120  
 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 DB 121 GAGGTCCGAGAGAAGTTCTCTGAGGGCCCATCCGTGTGTGAGCCAGCAGGAGCTGGGCCTC 180  
 QY 61 PheIleIysLeuLeuValGluAlaLeuGlyGlyGlyValAlaAsnProGluThrSerTrpThr 80  
 DB 181 CTATCAAGAGGTGGTGTGATGCCCTGGGGGGGGTGGGAGCCAGAACCAACTCGACC 240  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 DB 241 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGCAGCGCCTTCTTTTCTCAGGGACC 297  
 QY 101 IleIleThrThrIleGlyThrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 DB 298 ATCATCACCACCATCGCTATGCAATGTGGCCCTGCGCACAGATGCGGGCGCCTCTTC 357  
 QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
 DB 358 TGCATCTTTTATGCTGTGGGGATTCGCTGTGGGATCTTACTGGCAGGGGTCGGG 417  
 QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 DB 418 GACCGGCTGGGCTCTCTCCCTGGCCATGGCATCGGTACATTCAGGCATCTTCTTGAAG 477  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180

DB 478 TGGCAGCTGCCACCGGAGCTAGTAAGAGTGTGTGGCGATGCTTTCTGTGATCGGC 537  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyMetGluSerTrpSerLys 200  
 DB 538 TGCCTGCTCTTTGTCTCCTACGCCACGTTCTGTCTGTATATGAGGACTGGAGCAAG 597  
 QY 201 LeuGluAlaIleTyPheValIleValThrLeuThrThrValGlyPheGlyAspTrpVal 220  
 DB 598 CTGGAGGCACTTACTTGTCTAGTACGCTTACCACCGTGGGCTTTGGCGCATATGTG 657  
 QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyGlnProLeuValTrpPheTrpIle 240  
 DB 658 GCCGGCGCGGACCCACGAGGAGACTCCCGGCTATCAGCGCTGTGTGTTCTGGATC 717  
 QY 241 LeuPheGlyLeuAlaTyPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
 DB 718 CTGCTCGGCTTGGCTTACTTTCCTCAGTGTCTCACCACCATCGGAATGGCTGCGAGTA 777  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 DB 778 GTGTCCCGCGCACCTCGGCAGAGATGGCGGCTCAGCGCTCAGCTGCGAGCTGGACT 837  
 QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 DB 838 GGCACAGTCACAGCGCGCTGACCCAGCAGCGCGGCGCCGCCCGCCCGCGGAGAG 897  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320  
 DB 898 GAGCAGCCACTG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 945  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 DB 946 AGGCCCGCATCCCTTCGCGCCCGCAGAGAGCTCAGCGCCTTCCCGCGCCACGGCTCG 1005  
 QY 341 AlaLeuAspTyProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
 DB 1006 GCCCTGGATTATCCGAGCAGAACCTTGGCTTTCATCAGAGTCTTCGGATACGAGAC 1065  
 QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380  
 DB 1066 GAGCGCGCTGCCCTGCGCGCGCGAGAGGTGCGCGCGCCCAATCCCGCCAGG 1125  
 QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
 DB 1126 AAGCCCGTGGCGG 1179

RESULT 3  
 AAH78636  
 ID AAH78636 standard; cDNA; 1182 BP.  
 XX AC AAH78636;  
 XX DT 10-DEC-2001 (first entry)  
 XX DE Human mechanically sensitive potassium channel hTRAAK cDNA.  
 XX Human; mechanically sensitive potassium channel; riluzole; TWICK;  
 KW polyunsaturated fatty acid; arachidonic acid; hTRAAK; chromosome 11q13;  
 KW neuronal excitation; muscle excitation; cardiac rhythm; anoxia;  
 KW hormone secretion; cardiac disease; vascular disease; ischemia;  
 KW nervous system disorder; endocrinal disease; muscle disease;  
 KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1. .1182  
 FT /tag= a  
 FT /product= "mechanically sensitive potassium channel  
 FT hTRAAK"  
 XX WO200168670-A2.  
 XX

PD 20-SEP-2001.  
XX 14-MAR-2001; 2001WO-FR000758.  
XX 14-MAR-2000; 2000FR-00003264.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX Lazdunski M, Lesage F, Maingret F;  
XX WPI; 2001-590037/66.  
XX P-PSDB; AAG67777.  
XX New mechanically sensitive potassium channel, useful for treating  
XX cardiovascular diseases and in drug screening, is activated by  
XX polyunsaturated fatty acids.  
XX Claim 4; Page 32-33; 37pp; French.  
XX The present sequence encodes a human mechanically sensitive potassium  
XX channel which is activated by polyunsaturated fatty acids (particularly  
XX arachidonic acid (AA)) and by riluzole. The polypeptide is designated  
XX human TWICK-related AA-activated potassium channel (hTRAAK). The hTRAAK  
XX gene is located on chromosome 11q3. hTRAAK is involved in regulation of  
XX neuronal and muscle excitation, cardiac rhythm and secretion of hormones.  
XX Cells that express hTRAAK, designated to screen for modulators of hTRAAK  
XX activity. Such modulators are potentially useful for prevention or  
XX treatment, in humans and animals, of: cardiac and/or vascular disease;  
XX nervous system disorders associated with ischemia and anoxia; endocrinal  
XX diseases associated with anomalous hormone secretion or muscle diseases;  
XX and retinal diseases. Typical examples are epilepsy, cardiac arrhythmia  
XX and neurodegeneration  
XX Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 U; 0 Other;  
XX

Alignment Scores:  
Pred. No.: 3,44e-84 Length: 1182  
Score: 1692.50 Matches: 328  
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Query Match: 81.41% Indels: 5  
DB: 4 Gaps: 2

US-09-655-272-2 (1-398) x AAH78636 (1-1182)  
QY 1 MetArgSerThrThrLeuLeuAlaLeuAlaLeuValLeuLeuTyrLeuValSerGly 20  
Db 1 ATGGCAGCACCACCGCTCTGGCCCTCTGGCGCTGGTCTTGTCTTATCTTGTGTCTGGT 60  
QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
Db 61 GCCTCGGTGTTCGGGCGCTTGGAGCAGCCACGAGCAGCGCCACGAGGAGCTGGGG 120  
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
Db 121 GAGTCCGAGAGAAGTTCTGAGGGGCCATCGGTGTGTGAGCGACGAGAGCTGGGCTC 180  
QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTyrThr 80  
Db 181 CTCATCAAGGAGGTGGTGTATGCCCTTGGAGGGGGTGGCGACCCAGAACCACTCGACC 240  
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
Db 241 AGCAACAGCAGCAC--TCAGCTGGACCTGGGCGAGCGCTTCTTTCTTCAGGGACC 297  
QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyValLeuPhe 120  
Db 298 ATCATCACCACTCGCTATGGCAATGTGGCCCTCGCCACAGATCGCGGGCGCTCTTC 357  
QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
Db 358 TGCATCTTTTATGGCTGGTGGGATTCCTGCTTGGGATCTCTACTGGCAGGGTGGG 417

QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
Db 418 GACCGGTGGCTCTCCCTCCCTGCGCCATGCAATCGTGCATTTGAAG 477  
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180  
Db 478 TGGCACGTGCCACCGGAGCTAGTAAGAGTCTGTGCGCATGCTTTCTCTGCTGATCGGC 537  
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTyrSerLys 200  
Db 538 TGCCTGTCTCTTTGTCTTCACGCCCATGTTCTGTCTGTATATGAGGACTGGAGCAAG 597  
QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220  
Db 598 CTGAGGCCATCTACTTTGTCTAGTGTACACCGTGGCTTGGCGACTATGTG 657  
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTyrPheTyrIle 240  
Db 658 GCCGCGCGGACCCAGCGAGACTCCCCCGCTATCAGCGCTGTGTGTGTGATC 717  
QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
Db 718 CTGCTCGGCTGGCTTACTTCGCTCAGTGTCCACCATCGGAACCTGCTCGAGTA 777  
QY 261 ValSerArgArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTyrThr 280  
Db 778 GTGTCCGCGCACTCGGGCAGAGATGGCGGCTCAGCGCTCAGGCTGCAGCTGGACT 837  
QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
Db 838 GGCACAGTGAGCAGCGCGCTGACCCAGCGAGCGCGCGCGCGCGCGCGAGAG 897  
QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320  
Db 898 GAGCAGCCACTG-----CTGCTCCACCGCTGTCCAGCGCAGCCGCTGGGC 945  
QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340  
Db 946 AGGCGCGGATCCCTTCGCGCCCGCGAGAGGCTAGCGCGCTTCCCGCCCGCGCTCG 1005  
QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
Db 1006 GCCTCGATTATCCAGCGAGAACCTGCGCTTCATCGACGAGTCTCTCGGATACGAGAGC 1065  
QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgGlyArgProAsnProSerLys 380  
Db 1066 GAGCGCGGTGCGCGCTGCGCGCGCGCGAGAGTCCGCGCGCGCGCGCGCGCGCGAGG 1125  
QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
Db 1126 AGCCCGTGGCGGTG 1179

RESULT 4  
AAA27106  
ID AAA27106 standard; cDNA; 1218 BP.  
XX  
XX AAA27106;  
AC  
XX 04-AUG-2000 (first entry)  
DT  
XX  
XX Human h-TRAAK cDNA sequence #2.  
DE  
XX Human; h-TRAAK; potassium channel polypeptide;  
KW 2P domain potassium channel; neurodegenerative disease; stroke;  
KW psychiatric disorder; neurological disorder; Gene therapy; ss.  
XX  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 37..1218  
FT /\*tag= a  
FT /product= "h-TRAAK protein #2"  
XX

PN WO200026253-A1.  
 XX 11-MAY-2000.  
 XX 03-NOV-1999; 99WO-GB003634.  
 XX 03-NOV-1998; 98GB-00024048.  
 PR 07-OCT-1999; 99GB-00023668.  
 XX (SMIK ) SMITHLINE BERCHAM PLC.  
 PA Chapman CG, Duckworth DM;  
 PI WPI; 2000-365583/31.  
 DR P-PSDB; AAY94426.  
 XX Novel isolated h-TRAAK polypeptides belonging to the potassium channel  
 PT family of polypeptides, useful for the diagnosis and treatment of h-TRAAK  
 PT related disorders, e.g. depression and schizophrenia.  
 XX Claim 11; Page 21 and 22; 35pp; English.  
 PS  
 CC Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK  
 CC polynucleotides from human tissue samples. h-TRAAK polypeptides have  
 CC homology to the 2P domain potassium channel family of polypeptides. The h  
 CC -TRAAK polypeptides and polynucleotides may be used in diagnostic assays  
 CC for conditions related to h-TRAAK imbalance and for identifying agonists  
 CC and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and  
 CC polynucleotides may also be useful for treatment and prevention (e.g. as  
 CC vaccines) of certain diseases, such as pain, psychiatric disorders  
 CC including depression and schizophrenia, neurodegenerative disease  
 CC including Alzheimer's, stroke and head trauma and neurological disorders  
 CC including migraine and epilepsy. The present sequence is human h-TRAAK  
 CC cDNA sequence #2  
 XX  
 SQ Sequence 1218 BP; 182 A; 421 C; 395 G; 220 T; 0 U; 0 Other;  
  
 Alignment Scores:  
 Pred. No.: 3,546-84 Length: 1218  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 89.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5  
 DB: 3 Gaps: 2  
  
 US-09-655-272-2 (1-398) x AAA27106 (1-1218)  
  
 QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20  
 DB 37 ATGCGCAGCACCACGCTCTGGCCCTGCTGGCGCTGCTTGTCTTGTCTGTCTGT 96  
 QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
 DB 97 GCCTCTGTGTTCCGGGCCCTGGAGCAGCCGCCACAGCAGCAGCAGCAGGAGGAGCTGGGG 156  
 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 DB 157 GAGGTCGAGAGAAGTTCCTGAGGGCCCATCCGTGTGTGAGCAGCAGCAGGAGCTGGCCCTC 216  
 QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
 DB 217 CTCATCAAGGAGGTGGCTGATGCCCTGGGAGGGGGTGGGAGCCACGAAACCACTCGACC 276  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 DB 277 AGCAACAGCAGCCAC---TCAGCCTGGACCTGGGAGGCCCTCTCTTTCTCAGGAGACC 333  
 QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 DB 334 ATCATCACCACTCGGCTATGCAATGTGGCCCTGGCAGACAGATGCCGGGGCCCTCTTC 393  
 QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140

DB 394 TGCATCTTTATGCGCTGTGGGATTCGCTGTTTGGGATCTACTGCGAGGGGTCTGGG 453  
 QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGlyAlaIlePheLeuLys 160  
 DB 454 GACCGGCTGGGCTCTCTCCCTGCGCCATGCGATCGGTACATTAAGCCATCTCTTTGAAG 513  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180  
 DB 514 TGGCAGCTGCCACCGAGCTAGTAAGAGTGTGTGCGCATGCTTTTCTGTGATCGGC 573  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
 DB 574 TGCCTGCTCTTTGTCTCAGCCCATGCTGCTGCTTCTGTATATGAGGACTGAGACGAG 633  
 QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220  
 DB 634 CTGGAGGCCATCTACTTTGTATAGTACGCTTACCACGCTGGGCTTGGCGACTATGTG 693  
 QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240  
 DB 694 GCGGCGCGGAGCCCGCAGGAGGACTCCCGGCTATCAGCCGCTGTGTGTCTGGATC 753  
 QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
 DB 754 CTGCTCGGCTGGCTTACTTTCCTCAGTGTCTACCCATCGGAACTGGCTCGAGTA 813  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 DB 814 GTGTCCCGCGCACCTCGGCGAGAGATGGCGGCTCAGGCTCAGGCTGCCAGCTGGACT 873  
 QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 DB 874 GGCACAGTGACAGCGCGTGCACCCAGCAGCGCGGCGCGCGCGCGCGCGCGGAGAG 933  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320  
 DB 934 GAGCAGCCACTG-----CTGCCCTCAGCCGCTGTCCAGCGCGCGCTGGGC 981  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 DB 982 AGGCCCGGATCCCTTCGCCCCCGAGAGGCTCAGCGGCTTCCCGCGCCAGCGCTCG 1041  
 QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerSerThrGlnSer 360  
 DB 1042 GGCCTGGATTATCCAGCGAGAACCTGGCTTTCATCGAGAGTCTCTCGGATACGAGAGC 1101  
 QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProSerLys 380  
 DB 1102 GAGCGGCTGCGCGCTGCGCGCGCGGAGAGGTGCGCGCGCGCGCGCGCGCGCGAGG 1161  
 QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
 DB 1162 AAGCCGTCGCGCGCGCGCGCGCGCGCGCTCCCGGAGACAAAGGCGTGGCGGTG 1215  
  
 RESULT 5  
 AAH99922  
 ID AAH99922 standard; cDNA; 1257 BP.  
 XX  
 AC AAH99922;  
 XX  
 DT 25-JAN-2002 (first entry)  
 XX  
 DE Nucleotide sequence of human TWIK-8 receptor channel.  
 XX Human; potassium channel; transmembrane domain: TWIK; TWIK-8;  
 KW Tandem of P domain in a Weak Inward rectifying K<sub>v</sub> channel; K<sub>v</sub>;  
 KW central nervous system disorder; cardiovascular disease;  
 KW potassium channel mediated disorder; Alzheimers disease;  
 KW Parkinsons disease; multiple sclerosis; Picks disease;  
 KW neurodegenerative disorder; Lewy diffuse body disease; senile dementia;  
 KW Huntingtons disease; movement disorder; epilepsy; AIDS related dementia;  
 KW Gilles de la tourettes syndrome; amyotrophic lateral sclerosis;  
 KW progressive supranuclear palsy; Jakob-Creutzfeldt disease;



KW autonomic function disorder; neuropsychiatric disorder; phobia;  
 KW bipolar affective disorder; ss; nootropic; neuroprotective;  
 KW antiparkinsonian; antiarteriosclerotic; cyostatic; hypotensive;  
 KW antidepressant; antimigraine; analgesic; vasotropic; anticonvulsant;  
 KW neuroprotective; tranquilizer; neuroleptic; cancer;  
 KW learning and memory disorder; cell proliferation disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1. .1257  
 FT /\*tag= a  
 FT /product= "human TWIK-8"  
 FT /partial  
 FT /note= "No stop codon"  
 XX  
 XX WO200177329-A2.  
 XX  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-US011301.  
 XX  
 XX 07-APR-2000; 2000US-0195734P.  
 XX  
 XX (WILL-) MILLENIUM PHARM INC.  
 XX  
 XX Gluckemann WA;  
 XX  
 XX WPI; 2002-010911/01.  
 XX  
 XX P-PSDB; AAG78406.  
 XX  
 XX Novel isolated 12303, a human tandem of P domains in a weak inward  
 XX rectifying potassium channel-related potassium channel subunit  
 XX polypeptide useful for treating Alzheimer's disease, restenosis, migraine  
 XX and cancer.  
 XX  
 XX Claim 1; Page 122-124; 124pp; English.  
 XX  
 XX This invention relates to a human TWIK-8 (tandem of P domains in a weak  
 XX inward rectifying K<sup>+</sup> channel)-related potassium channel subunit  
 XX polypeptide. Applications of the polypeptide include: nootropic,  
 XX neuroprotective, antiparkinsonian, antiarteriosclerotic, cyostatic,  
 XX hypotensive, antidepressant, antimigraine, analgesic, vasotropic,  
 XX anticonvulsant, neuroprotective, tranquilizer, neuroleptic, in gene  
 XX therapy, and as a modulator of potassium channel mediated activity in a  
 XX cell, and is useful in screening assays, detection assays, predictive  
 XX medicine and in methods of treatment. The polypeptide is useful as a  
 XX target for developing modulating agents to regulate a variety of cellular  
 XX processes, and is also useful as query sequence to perform a search  
 XX against public databases to, for example, identify other family members  
 XX or related sequences. The polypeptide is useful for treating disorders  
 XX characterized by insufficient or excessive production of TWIK-8 protein  
 XX or production of TWIK-8 protein forms which have decreased, aberrant or  
 XX unwanted activity compared to TWIK-8 wild type protein, e.g., potassium  
 XX channel associated disorders including central nervous system disorders  
 XX such as cognitive and neurodegenerative disorders, autonomic function  
 XX disorders, learning or memory disorders, cardiac disorders, muscular  
 XX disorders, pain disorders and disorders of cellular growth,  
 XX differentiation or migration. The polypeptide is useful as immunogen to  
 XX raise anti-TWIK-8 antibodies, and to screen for drugs, and is also  
 XX considered useful for producing non-human transgenic animals. This  
 XX sequence represents the nucleotide sequence for human TWIK-8, which  
 XX differs to the sequence in AAH99922 since it does not contain the 3',  
 XX untranslated region  
 XX  
 XX Sequence 1257 BP; 188 A; 443 C; 404 G; 222 T; 0 U; 0 Other;  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 3,66e-84 Length: 1257  
 XX Score: 1692.50 Matches: 328  
 XX Percent Similarity: 88.44% Conservative: 24  
 XX Best Local Similarity: 82.41% Mismatches: 41  
 XX Query Match: 81.41% Indels: 5

DB: 6 Gaps: 2  
 US-09-655-272-2 (1-398) x AAH99922 (1-1257)  
 QY 1 MetArgSerThrLeuLeuAlaLeuAlaLeuValLeuLeuValSerGly 20  
 DB 79 ATGGCAGACACACGCTCTGGCCCTGCTGGCGCTGGTCTGTCTTACTTGGTCTGGT 138  
 QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
 DB 139 GCCCTGGTGTCCGGGCGCTGGAGCAGCCACAGCAGCAGGAGCCAGAGGAGCTGGG 198  
 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluasp 60  
 DB 199 GAGGTCCGAGAGAAATTCCTGAGGGCCCATCCGTGTGTGAGCAGCAGGAGCTGGGCTC 258  
 QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
 DB 259 CTCATCAAGGAGGTGGTGTATGCCCTGGAGGGGTGGGACCCAGAAACCACTCGACC 318  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 DB 319 AGCAACACAGCCAC---TCAGCCTGGGACCTGGGCGAGCGCTTCTTTTCTCGAGGACC 375  
 QY 101 IleIleThrThrIleGlyTyrglyValIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 DB 376 ATCATCACCCATCGGCTATGGCAATGTGGCCCTGGCGCAGATGCCGGCGGCTCTTC 435  
 QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
 DB 436 TGCATCTTTATGCTGCTGGTGGGATTCGGCTGTTGGGATCTTACTGCGAGGGGTGGG 495  
 QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 DB 496 GACCGCTGGGCTCCTCCCTCGCCATGGCATCGGTCTCATTTGAAGCCATCTTCTTGAG 555  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180  
 DB 556 TGGCAGCTGCCACCGGAGCTAGTAAGAGTGTGTGCGGATGCTTTTCTGCTGATCGG 615  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
 DB 616 TGCCTGCTTTTGTCTCTCAGCCGCCAGTTCGTGTCTGTCTATATGAGGACTTGGAGCA 675  
 QY 201 LeuGluAlaIleTyrglyPheValIleValThrLeuThrValGlyPheGlyAspTrpVal 220  
 DB 676 CTGGAGGCCATCTACTTTGTCTAGTACGCTTACCCGCGGGCTTTGGCGACTATGTG 735  
 QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrglnProLeuValTrpPheTrpIle 240  
 DB 736 GCCGGCGCGGACCCCGAGGAGGACTCCCGGCTATCAGCCGCTGGTGTGGTCTTGATC 795  
 QY 241 LeuPheGlyLeuAlaTyrglyPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
 DB 796 CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTCACCACCATCGGAACTGGCTGGAGTA 855  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 DB 856 GTGTCCCGCGCACTCGGCGAGAGTGGCGGCGCTCACGGCTCAGGCTCCAGCTGGACT 915  
 QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 DB 916 GGCACAGTGCACGGCGGTGACCCAGCGCGGCGCGCGCGCGCGCGCGCGCGGAGAAG 975  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320  
 DB 976 GAGCAGCCACTG-----CTGCCTCCACCGCCCTGTCCAGCGCGCGCTGGGC 1023  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 DB 1024 AGGCCCGCATCCCTTCGCCCCCGGAGAGGCTCAGCCGCTTCCCGCGCCACCGGCTCG 1083  
 QY 341 AlaLeuAspTyrglyProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360



Db 676 CTGAGGCCATCTACTTTGTCTATAGTACGCTTACCACCGTGGCTTTGGCGACTATGTG 735  
 QY 221 ProGlyAspGlyThrGlyGlnAenSerProAlaTyxGlnProLeuValTrpPheTrpIle 240  
 Db 736 GCCGGGCGGACCCAGGAGGACTCCCGGCTATACGCGCTGTGTGTTCTGGATC 795  
 QY 241 LeuPheGlyLeuAlaTyxPheAlaSerValLeuThrThrIleGlyAenTrpLeuArgAla 260  
 Db 796 CTGCTCGGCTGGCTTACTTGGCTCTCAGTGCTCACCACCATCGGAACCTGGCTCGGAGTA 855  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaSerTrpThr 280  
 Db 856 GTCTCCGCGCCACTCGGGCAGAGATGGCGGCTCAGCGCTCAGCTGCCAGCTGGACT 915  
 QY 281 GlyThrValThrAlaArgValThrGlnAtrThrGlyProSerAlaProProGluLys 300  
 Db 916 GGCACAGTACACGGCGGTGACCCAGCGCGGCGCGCGCGCGCGCGCGCGCGGAG 975  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320  
 Db 976 GAGCAGCCACTG-----CTGCTCCACCGCGCTGTCTCAGCGCAGCGCTGGGC 1023  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 Db 1024 AGCCCGGATCCCTTGGCCCCCGGAGAGGCTCAGCGCGCTTCCCGCCACGCGCTCG 1083  
 QY 341 AlaLeuAspTyxProSerGluAenLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
 Db 1084 GCCTTGATATCCAGCGAGAACCTTGGCTTCATCGACGAGTCTTCGGATAGCGAGAGC 1143  
 QY 361 GluArgGlyCysAlaLeuProAlaProAlaProAlaProAlaProAlaProAlaProAla 380  
 Db 1144 GAGCGCGCTGCCCGTCCCGCGCGCGCGGAGAGTCCGCGCGCCCAATCCCGCCAGC 1203  
 QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
 Db 1204 AAGCCCGTGGCGGTG 1257  
 RESULT 7  
 ID ADH51640 standard; DNA; 1260 BP.  
 XX ADH51640;  
 AC ADH51640;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Human 12303 protein coding DNA sequence.  
 XX  
 KW cytotatic; vasotropic; haemostatic; nephrotropic; gastrointestinal-Gen;  
 KW respiratory-Gen; muscular-Gen; osteopathic; antiinflammatory;  
 KW immunosuppressive; cardiovascular-Gen; hepatotropic; virucide; analgesic;  
 KW antianaemic; endocrine-Gen; neuroprotective; nontropic; cardiatic;  
 KW gene therapy; cellular proliferative; differentiative disorder; brain;  
 KW blood vessel; platelet; breast; colon; kidney; lung; ovarian; prostate;  
 KW pancreatic; skeletal muscle; testicular; hormonal; bone metabolism;  
 KW immune disorder; inflammatory disorder; cardiovascular disorder;  
 KW endothelial cell; liver; viral; pain; metabolic; anaemia; angiogenesis;  
 KW neoplastic; endocrine disorder; neurological; heart; tissue typing;  
 KW chromosomal mapping; predictive medicine; pharmacogenomic; human; gene;  
 DB; 12303.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003219806-A1.  
 XX  
 PD 27-NOV-2003.  
 XX  
 PF 18-MAR-2003; 2003US-00391399.  
 XX  
 PR 22-FEB-2000; 2000US-00510706.  
 PR 07-APR-2000; 2000US-0395734P.  
 PR 31-MAY-2000; 2000US-00583373.  
 PR 26-JUN-2000; 2000US-0214176P.

PR 08-AUG-2000; 2000US-00634669.  
 PR 31-AUG-2000; 2000US-0229036P.  
 PR 19-SEP-2000; 2000US-0233537P.  
 PR 01-FEB-2001; 2001US-0267076P.  
 PR 20-FEB-2001; 2001US-00789481.  
 PR 12-MAR-2001; 2001US-0275078P.  
 PR 12-MAR-2001; 2001US-0275172P.  
 PR 06-APR-2001; 2001US-00828035.  
 PR 26-JUN-2001; 2001US-00891762.  
 PR 29-AUG-2001; 2001US-00942447.  
 PR 17-SEP-2001; 2001US-0322983P.  
 PR 19-SEP-2001; 2001US-00957685.  
 PR 27-SEP-2001; 2001US-0325854P.  
 PR 04-DEC-2001; 2001US-0336936P.  
 PR 31-JAN-2002; 2002US-00062937.  
 PR 08-MAR-2002; 2002US-00094214.  
 PR 11-MAR-2002; 2002US-00095139.  
 PR 17-SEP-2002; 2002US-00245121.  
 PR 26-SEP-2002; 2002US-00255532.  
 PR 04-DEC-2002; 2002US-00309804.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Glucksmann MA, Curtis RAJ, Lora JM, Galvin KM, Silos-Santiago I;  
 PI P-PSDB; ADH51639.  
 XX  
 DR WPI; 2004-010868/01.  
 DR  
 XX  
 XX  
 PT New 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324,  
 PT 55063, 52991, 59914, 59921 or 33751 nucleic acid molecule or polypeptide,  
 PT useful for diagnosing, preventing or treating e.g. proliferative or brain  
 PT disorders.  
 XX  
 PS Claim 1; SEQ ID NO 20; 276pp; English.  
 XX  
 CC This invention relates to novel human DNA sequences (designated 18607,  
 CC 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063,  
 CC 52991, 59914, 59921 or 33751) and the proteins encoded by them. The  
 CC invention may be useful for the development of compounds with a  
 CC cytotatic, vasotropic, haemostatic, nephrotropic, gastrointestinal-Gen,  
 CC respiratory-Gen, muscular-Gen, osteopathic, antiinflammatory,  
 CC immunosuppressive, cardiovascular-Gen, hepatotropic, virucide, analgesic,  
 CC antianaemic, endocrine-Gen, neuroprotective, nontropic or cardiatic  
 CC activity. In addition, the sequences may be useful for gene therapy. The  
 CC invention may be useful in diagnosing, preventing or treating disorders  
 CC characterised by aberrant 18607, 15603, 69318, 12303, 48000, 52920, 5433,  
 CC 38554, 57301, 58324, 55063, 52991, 59914, 59921 or 33751 activity, for  
 CC example cellular proliferative and/or differentiative disorder, brain  
 CC disorder, blood vessel disorder, platelet disorder, breast disorder,  
 CC colon disorder, kidney disorder, lung disorder, ovarian disorder,  
 CC prostate disorder, pancreatic disorder, skeletal muscle disorder,  
 CC testicular disorder, hormonal disorder, disorder associated with bone  
 CC metabolism, immune disorder, inflammatory disorder, cardiovascular  
 CC disorder, endothelial cell disorder, liver disorder, viral disease, pain,  
 CC metabolic disorder, anaemia, angiogenesis disorder, neoplastic disorder,  
 CC endocrine disorder, neurological disorder or heart disorder. They may  
 CC also be used in screening assays, tissue typing, chromosomal mapping,  
 CC predictive medicine or pharmacogenomics. The present sequence is that of  
 CC the coding DNA sequence for the human 12303 protein of the invention.  
 XX  
 SQ Sequence 1260 BP; 189 A; 443 C; 405 G; 223 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3,67e-84 Length: 1260  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 88.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5  
 DB: 12 Gaps: 2

US-09-655-272-2 (1-398) x ADH51640 (1-1260)

QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuTyrLeuValSerGly 20





```

PR 25-NOV-2002; 2002US-0429048P.
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX Carroll JM, Healy A, Weich NS, Kelly LM;
XX WPI; 2003-731464/69.
DR P-PSDB; ADK52550.
XX
XX Identifying a compound capable of treating a hematologic disorder (e.g.
PT anemia or leukemia) comprises assaying the ability of the compound to
PT modulate the expression or activity of e.g. 131.148, 199 or 12303
PT polypeptide or nucleic acid.
XX
XX Disclosure; SEQ ID NO 7; 232pp; English.
XX
XX The invention relates to a method of identifying a compound capable of
XX treating a hematologic disorder comprises assaying the ability of the
XX compound to modulate 131.148, 199, 12303, 13906, 15513, 17822, 302, 5677,
XX 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871,
XX 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8930 or 13249 nucleic
XX acid expression or polypeptide activity, thus, identifying a compound
XX capable of treating a hematologic disorder. The methods are useful in
XX diagnosing, preventing and treating hematological disorders, such as
XX cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia,
XX Polycythemia Vera, Lymphoma, Retinoblastoma, Hemophilia, disorders
XX associated with an increased risk of Thrombosis, Herpes, Thalassemia,
XX antibody-mediated disorders such as transfusion reactions and
XX Erythroblastosis, mechanical trauma to red blood cells such as micro-
XX angioathic hemolytic anemias, infections by parasites or chemical
XX injuries. The methods may also be used for identifying compounds that
XX modulate hematological disorders. This sequence corresponds to one of the
XX genes modulated the compound.
XX
XX SQ Sequence 1408 BP; 204 A; 500 C; 459 G; 245 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.12e-84 Length: 1408
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 10 Gaps: 2

US-09-655-272-2 (1-398) x ADK52549 (1-1408)

QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuValLeuValSerGly 20
DB 162 ATCGCAGCACCACGCTCCCTGGCCCTGCTGGCCCTGCTGGCTTGTCTTGTCTGTCTGTGT 221

QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40
DB 222 GCCTGTGTTCCTGGGCGCTTGGAGCAGCCACAGCAGCAGCAGCAGCAGGAGGAGTGGGG 281

QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
DB 282 GAGGTCGAGAGAAGTTCCTGAGGGGCCCATCCGTGTGTGAGCGACACAGGAGCTGGGCCCTC 341

QY 61 PheIleLysLeuValGluAlaLeuGlyGlyGlyValAlaAsnProGluThrSerTrpThr 80
DB 342 CTATCAAGAGGTGGTGGTCCCTGGGGGGGGTGGGAGCCAGAACCAACTCGACC 401

QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
DB 402 AGCAACAGCAGCAC--TCAGCTGGGACCTGGGAGCGCCCTCTTTTCTCAGGGACC 458

QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
DB 459 ATCATCACCACCATCGCTATGCAATGTGGCCCTGGCCACAGATGCGGGCGCCCTCTTC 518

QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
DB 519 TGCATCTTTTATCGCTGGGGGATTCGCTGTTTGGGATCTTACTTGGCAGGGGTGGGG 578

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QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 579 GACCGGCTGGGCTCCTCCCTGGCCCATGGCTGCGTCACTTGAAGCCATCTTCTTGAAG 638

QY 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
DB 639 TGGCAGTGGCCACCGGAGCTAGTAAGAGTGTGTGGCGCATGCTTTTCTGCTGATCGGC 698

QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
DB 699 TGCCTGCTCTTGTCTCTCAGCCGACGTTCTGTTCTGCTATATGAGGAGCTGGAGCAAG 758

QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTrpVal 220
DB 759 CTGGAGGCACTTACTTGTCTAGTACGCTTACCACCGTGGGCTTTGGCGCATATGTG 818

QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
DB 819 GCGGGCGCGGACCCAGGAGGAGTCCCGGCTATCAGCGCTGTGTGTGTCTGATC 878

QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
DB 879 CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTCACCACCATCGGAACCTGGCTCGAGTA 938

QY 261 ValSerArgArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
DB 939 GTGTCGCGCGCAGCTCGGCGAGAGATGGCGGCTCAGCGCTCAGCTGCCAGCTGACT 998

QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
DB 999 GGCACAGTACAGCGGCGGTGACCCAGCAGCGCGGCGCGCGCGCGCGCGCGCGAGAG 1058

QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
DB 1059 GAGCAGCCACTG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGCGCTGGGC 1106

QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340
DB 1107 AGCGCGGCTGCGGCTGCGCCCGCGAGAGGCTCAGCGGCTTCCCGCGCGCGCGCGCTCG 1166

QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
DB 1167 GCCTGGATTATCCAGCGAGAACCTGGCTTCATCAGAGTCTTCGATACGACGAGC 1226

QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380
DB 1227 GAGCGGCGTGGCGCTGCGCGCGCGCGAGAGTTCGCGCGCGCGCGCGCGCGCGCGAG 1286

QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
DB 1287 AAGCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTG 1340

RESULT 10
ADH51638
ID ADH51638 standard; cDNA; 1408 BP.
XX
XX AC ADH51638;
XX
XX DT 25-MAR-2004 (first entry)
XX
XX DE Human 12303 protein cDNA sequence.
XX
XX cytosolic; vasotropic; haemostatic; nephrotropic; gastrointestinal-Gen;
XX respiratory-Gen; muscular-Gen; osteopathic; antiinflammatory;
XX immunosuppressive; cardiovascular-Gen; hepatotropic; virucide; analgesic;
XX antianemic; endocrine-Gen; neuroprotective; nootropic; cardiac;
XX gene therapy; cellular proliferative; differentiative disorder; brain;
XX blood vessel; platelet; breast; colon; kidney; lung; ovarian; prostate;
XX pancreatic; skeletal muscle; testicular; hormonal; bone metabolism;
XX immune disorder; inflammatory disorder; cardiovascular disorder;
XX endothelial cell; liver; viral; pain; metabolic; anaemia; angiotensin;
XX neoplastic; endocrine disorder; neurological; heart; tissue typing;

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Db 439 ATCATCACCACTCGCTATGCAATGCGCTCGGCACAGATCCCGGGCGCTCTTC 498
Qy 121 CysilePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 499 TGCATCTTCTATGCTGCTGGGGATTCGCTGTTGGGATCCTACTGGCAGGGTCGG 558
Qy 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 559 GACCGGCTGGGCTCTCCCTCGGCCATGGCATCGGTACATTAAGGCCATCTCTTTGAAG 618
Qy 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180
Db 619 TGGCAGTGGCCACGGAGCTAGTAGAGTCTGTGGCGATGCTTTCTGCTGATCGGC 678
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 679 TGCCTGCTCTTTGCTCTCAAGCCACGCTTCTGCTATATGAGGAGCTGGAGCAAG 738
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
Db 739 CTGGAGGCCATCTACTTTGTATAGTACGCTTACCACCGTGGGCTTTGGCGACTATGTG 798
Qy 221 ProGlyAspGlyThrGlyGlnAenSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 799 GCCGGCGGACCCCGGAGGACTCCCGGCTATCAGCCGCTGGTGTGTTCTGATC 858
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAenTrpLeuArgAla 260
Db 859 CTGCTCGGCTGCTTACTTTCGCTCAGTGTCTACACCATCGGAATCGGCTGGAGTA 918
Qy 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaIleTrpThr 280
Db 919 GTCTCCCGCGCACTCGGGCAGAGATGGCGGCTCAGCGCTCAGGCTGCAGCTGCACT 978
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 979 GGCACAGTGCAGCGCGTGACCCAGCGCGGCGGCGGCGGCGGCGGCGGCGGAG 1038
Qy 301 GluGlnProLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 1039 GAGCAGCCACTG-----CTGCTCCACCGCGCTGTCCAGCGCAGCGCTGGGC 1086
Qy 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340
Db 1087 AGGCCCGCATCCGCTTTCGCGCCCGCAGAGGCTCAGCTGCTTCCCGCCACGGCTCG 1146
Qy 341 AlaLeuAspTyrProSerGluAenLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 1147 GCCTCGATTATCCAGCGAGAACCTGGGCTTTCATCGAGGCTCTCGGATACGACAGC 1206
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAenProSerLys 380
Db 1207 GAGCGGCTGCGGCTGCGCGCGCGCGGAGAGTTCGCGCGCCCAATCCCCCAGG 1266
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1267 AAGCCCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1320
```

## RESULT 13

ADP21365

ID ADP21365 standard; DNA; 2772 BP.

XX AC

XX ADP21365;

XX DT

XX 09-SEP-2004 (first entry)

XX DE

DE Gene KCNK4 for screening for cardiac therapeutic preparation.

XX KW

KW de; cardiac; gene therapy; cardiac therapeutic preparation;

KW KW

KW beta-adrenergic receptor antagonist; endothelial receptor antagonist;

KW KW

KW calcium channel antagonist; phosphodiesterase inhibitor;

KW KW

KW angiotensin converting enzyme inhibitor; heart failure.

XX XX

OS Homo sapiens.

XX PN

XX WO2004050894-A2.

XX PD

XX 17-JUN-2004.

XX PF

XX 26-NOV-2003; 2003WO-US037927.

XX PR

XX 27-NOV-2002; 2002US-0429379P.

XX PR

XX 31-DEC-2002; 2002US-0437051P.

XX PR

XX 31-DEC-2002; 2002US-0437102P.

XX PA

XX (ARTE-) ARTESIAN THERAPEUTICS INC.

XX PI

XX Bednarik DP;

XX DR

XX WPI; 2004-450738/42.

XX PT

XX Screening potential therapeutic compounds for cardiac therapeutic

XX PT

XX preparations, useful for treating heart failure in a subject, comprises

XX PT

XX contacting a sample of cell or tissue with a compound and detecting gene

XX PT

XX expression level.

XX PS

XX Claim 10; SEQ ID NO 39; 152pp; English.

XX CC

XX The invention relates to a method of screening potential therapeutic

XX CC

XX compounds for cardiac therapeutic preparations by contacting a sample

XX CC

XX comprising a cell or tissue with a potential therapeutic compound and

XX CC

XX detecting a level of expression of a gene that codes for a product

XX CC

XX encoded by a nucleic acid selected from 98 sequences given in the

XX CC

XX specification and its conservative variants, comparing the level of the

XX CC

XX expression of the gene to the level of expression of the gene in the

XX CC

XX absence of the compound, and identifying a potential therapeutic compound

XX CC

XX for use as a cardiac therapeutic preparation if the potential therapeutic

XX CC

XX compound affects the level of expression of the gene. The pharmaceutical

XX CC

XX composition or active agents (i.e., beta-adrenergic receptor antagonist,

XX CC

XX endothelial receptor antagonist, calcium channel antagonist,

XX CC

XX phosphodiesterase inhibitor, or angiotensin converting enzyme inhibitor)

XX CC

XX is useful for treating heart failure in a subject. This sequence

XX CC

XX represents one of the genes whose expression may be altered by the

XX CC

XX compounds detected by the screen of the invention.

XX SQ

XX Sequence 2772 BP; 521 A; 911 C; 868 G; 472 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8,27e-84 Length: 2772

Score: 1692.50 Matches: 328

Percent Similarity: 88.44% Conservative: 24

Best Local Similarity: 82.41% Mismatches: 41

Query Match: 81.41% Indels: 5

DB: 12 Gaps: 2

US-09-655-272-2 (1-398) x ADP21365 (1-2772)

Qy 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20

Db 142 ATGCGCAGCACCACGCTCCTGGCCCTGCTGGCGCTGCTTGTCTTGTCTGCTGCT 201

Qy 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAsp 40

Db 202 GCCCTGCTGTTCCGGGCGCTTGGAGCAGCCCCCAGCAGCAGCAGGAGGCTGGGG 261

Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60

Db 262 GAGGTCGAGAGAGTTCCTGAGGGGCCCATCCGTGTGTGAGCGACCCAGGAGCTGGGCTC 321

Qy 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyAlaAenProGluThrSerTrpThr 80

Db 322 CTCATCAAGAGGTGGCTGATGCCCTGGGAGGGGTGGCGACCCAGAAACCACTGCACC 381

Qy 81 AenSerSerAsnHisSerSerAlaTrpAenLeuGlySerAlaPhePheSerGlyThr 100

Db 382 AGCAACAGCAGCCAC---TCAGCCTGGGACCTGGGCGGCGCTTCTTTTCTCAGGACC 438

Qy	101	IleIleThrThrIleGlyTyrGlyAsnIleValLeuLeuHieThrAspAlaGlyArgLeuPhe	120	KW	hormonal dysfunction; neoplasm; atherosclerosis; diabetes; chemotherapy;
Db	439	ATCATCACCAATCGGCTATGCAATGGCCCTCGGCACAGATCCCGGGCGCTTC	498	KW	anaemia; irradiation; erythroid precursor; erythroid cell; ulcer; organ;
Qy	121	CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly	140	KW	pressure ulcer; vascular insufficiency; surgical wound; traumatic wound;
Db	499	TGCATCTTTATGCGTGGTGGGATTCGCTGTGGGATCTACTCGCAGGGGTCGG	558	KW	pancreas; liver; intestine; kidney; skin; endothelium; skeletal muscle;
Qy	141	AspArgGlySerSerLeuArgArgGlyIleGlyHieIleGluAlaIlePheLeuLys	160	OS	smooth muscle; cardiac muscle; vascular tissue.
Db	559	GACCGCTGGGCTCTCCCTCGCCATGCGTACATTCGATTCGATTCGATTCG	618	XX	Homo sapiens.
Qy	161	TrpHisValProGlyIleValArgSerLeuSerAlaValLeuPheLeuLeuGly	180	PN	US2002146692-A1.
Db	619	TGCACGTGCCACCGAGCTAGTAAGAGTGTGCGGATGCTTCCTGCTGATCGGC	678	PD	10-OCT-2002.
Qy	181	CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys	200	PF	21-DEC-2000; 2000US-00747835.
Db	679	TGCTGCTCTTCTCTCAGCCACCGTTCGTCTATATGAGGACTGGAGCAAG	738	XX	21-JAN-2000; 2000US-00488725.
Qy	201	LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal	220	PR	25-APR-2000; 2000US-00552317.
Db	739	CTGGAGGCCATCTACTTGTCTATAGTACGCTTACCACCGTGGGCTTGGCGACTATGTG	798	PR	20-JUN-2000; 2000US-00598042.
Qy	221	ProGlyAspGlyThrGlyGlnAenSerProAlaTyrGlnProLeuValTrpPheTrpIle	240	PR	19-JUL-2000; 2000US-00620312.
Db	799	GCCGGCGGACCCAGGAGAGTCTCCCGGCTATCAGCGCTGTGTGTTCTGATC	858	PR	31-AUG-2000; 2000US-00653450.
Qy	241	LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla	260	PR	04-DEC-2000; 2000US-00729739.
Db	859	CTGCTGGGCTGCTTACTTCTGCTCAGTCTCAGTCTCACCACCATCGGAATGGCTCGAGTA	918	XX	(YAMA/) YAMAZAKI V.
Qy	261	ValSerArgArgThrArgAlaGluMetGlyIleuThrAlaGlnAlaSerTrpThr	280	PA	(TANG/) TANG Y T.
Db	919	GTGTCCCGCGCATCTCGGCGAGATGGCGGCTCAGCGCTCAGGCTGCCAGCTGACT	978	PA	(LIUC/) LIU C.
Qy	281	GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys	300	PA	(ZHOU/) ZHOU P.
Db	979	GGCACGTGACGGCGCTGACCCAGCGAGCGCGGCGCCCGCGCGCGGAGAG	1038	PA	(WANG/) WANG D.
Qy	301	GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly	320	PA	(ZHAN/) ZHANG J.
Db	1039	GAGCAGCACTG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGCGTGGC	1086	PA	(REN/) REN F.
Qy	321	ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer	340	PA	(ASUN/) ASUNDI V.
Db	1087	AGGCCCCGATCCCTTCCGCCCCCGAGAGGCTCAGCGGCTTCCCGCCCGACGGCTCG	1146	PA	(DRWA/) DRWANAC R T.
Qy	341	AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer	360	XX	Yamazaki V, Tang YT, Liu C, Zhou P, Wang D, Zhang J, Ren F;
Db	1147	GCCCTGTATATCCAGCGAGAACCTGCTTCATCCAGAGTCTTCGATACGAGC	1206	PI	Asundi V, Drmanac RT;
Qy	361	GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAnProSerLys	380	XX	WPI; 2003-174164/17.
Db	1207	GAGCGGCTGCGCGCTGCGCGCGCGCGAGAGTCTCGCGCGCCCAAAATCCCCCGAG	1266	XX	Isolated polynucleotide for treating, e.g. ophthalmic diseases, comprises
Qy	381	LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal	398	PT	specified nucleotide sequences, or their translated protein coding
Db	1267	AAGCCCGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG	1320	PT	portion, mature protein coding portion, extracellular portion, or active
DE	RESULT 14			XX	domain.
XX	ABX91950			XX	Claim 1; Page 100-102; 158pp; English.
AC	ABX91950;			CC	The invention relates to human G protein-coupled receptor-like (GPCR-
XX				CC	like) proteins and the polynucleotides encoding them. The isolated
XX				CC	sequences are used for the treatment of diseases of ophthalmic,
XX				CC	neurological, immunological, or nephritic systems. They may also be used
DT	08-MAY-2003 (first entry)			CC	to treat hormonal dysfunction, cancer and other neoplasia,
XX				CC	atherosclerosis, diabetes, in treating various anaemias or for use in
DE	Human G protein-coupled receptor-like (GPCR-like) cDNA #20.			CC	conjunction with irradiation/chemotherapy to stimulate the production of
XX				CC	erythroid precursors and/or erythroid cells. The sequences may be used to
KW	Human; G protein-coupled receptor; GPCR; gene; ss; ophthalmic disease;			CC	promote better or faster closure of non-healing wounds, including
KW	neurological disease; immunological disease; nephritic disease; cancer;			CC	pressure ulcers, ulcers associated with vascular insufficiency and
				CC	surgical and traumatic wounds and in generation or regeneration of other
				CC	tissues, e.g. organs (e.g. pancreas, liver, intestine, kidney, skin,
				CC	endothelium), muscle (smooth, skeletal, or cardiac) and vascular tissue
				CC	or for promoting the growth of cells comprising such tissues. Sequences
				CC	ABX91935-ABX91958 represent human GPCR-like polynucleotides of the
				CC	invention
				XX	Sequence 3945 BP; 606 A; 1344 C; 1238 G; 757 T; 0 U; 0 Other;
				SQ	
					Alignment Scores:
					Pred. No.: 1.97e-83 Length: 3945
					Score: 1688.50 Matches: 327
					Percent Similarity: 88.41% Conservative: 24
					Best Local Similarity: 82.37% Mismatches: 41
					Query Match: 81.22% Indels: 5
					DB: 8 Gaps: 2
					US-09-655-272-2 (1-398) x ABX91950 (1-3945)
					Qy 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20

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Db 1618 ATGGCAGCACCAGCTCCCTGGCCCTGCTGGCTGGCTGTCTGTCTTACTTTGGTGTCTGGT 1677
Qy 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGlnGlnAlaGlnLysLysMetAsp 40
Db 1678 GCCTGTGTTCGGGGCCCTGGAGAGCCACAGAGCAGAGCCGACAGAGGAGCTGGG 1737
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 1738 GAGTCCGAGAGAAGTTCTCTGAGGCCCATCCGTGTGTGAGACACACAGAGAGCTGGCCTC 1797
Qy 61 PheIleIysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 1798 CTATCAAGAGGTGTGATGCCCTGGAGGGGGTGGGACCCAGAAACAATCTGACC 1857
Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 1858 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGGACAGCCCTCTTTTCTCAGGGACC 1914
Qy 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 1915 ATCATCACCAACCATCGGCTATGCAATGTGGCCCTGCGCACAGATGCCGGGCGCCTTTC 1974
Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 1975 TGATCTTTTATGCTGTGGTGGGATTCCTGCTGTTGGATCCTACTGGCAGGGGTGGG 2034
Qy 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 2035 GACCGGCTGGCTCTCTCCCTGGCCATGGCATCGGTACATTCAGGCCATCTTCTGAAG 2094
Qy 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 2095 TGGCAGCTGTCACCGGAGCTAGTAAGAGTCTGTCGGCGATGCTTTTCTGCTGATCGGC 2154
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 2155 TGCTGTCTCTTGTCTCAGCCACCGTTCGTGTTCTGTATATGAGAGACTGGAGCAAG 2214
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
Db 2215 CTGGAGCCATCTACTTGTATAGTAGACCTTACACACCTGGGCTTGGCGACTATGTG 2274
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 2275 GCCGGCGCGACCCAGCAGGACTCCCGGCGCTATCAGCGCTGTGTGTCTGGATC 2334
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 2335 CTGCTCGGCTGTGCTTACTTTCGCTCAGTGTCTCAGTGTCTCAGTGTCTGCGAGTA 2394
Qy 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 2395 GTGTCCCGCGCACTCGGCGAGAGATGGGGCGCTCAGGCTCAGGCTGCAGCTGGACT 2454
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 2455 GGCACAGTGCAGCGCGGTGACCCAGCAGCGGGGCGCCCGCCGCGCGCGCGAGAG 2514
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320
Db 2515 GAGCAGCCACTG-----CTGCCCTCCAGCCGCTGTCCAGCGCAGCGCTGGGC 2562
Qy 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340
Db 2563 AGSCCCGATCCCTTCGCCCCCGAGAGGCTCAGCGGCTTCCCGCCGACGCGCTCG 2622
Qy 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 2623 GCCCTGGATTATCCAGCAGAGAACCTGGCCTTCATCGACGAGTCTTCGGATACGACAGC 2682
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAnProSerLys 380
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Db 2683 GAGCGCGGTGCTCCCGCTGCTCCCGCGCGAGAGGTGCGCGCCCAATCCCCAGG 2742
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValPro 397
Db 2743 AAGCCCGTGGCGGCCCGCGCGCGCGCGCTCCCGAGACAAAGCGGTGCGG 2793

RESULT 15
AAS08652
ID AAS08652 standard; cDNA; 3996 BP.
XX
AC AAS08652;
XX
DT 17-DEC-2001 (first entry)
DE
XX Human cDNA encoding G-protein coupled receptor like protein, GPCR #8.
XX Human; G-protein coupled receptor like protein; GPCR; immunogen;
XX ophthalmic disease; neurological disease; Alzheimer's disease;
XX Parkinson's disease; immunological disorder; HIV; candidiasis;
XX human immunodeficiency virus; autoimmune disorder; multiple sclerosis;
XX systemic lupus erythematosus; rheumatoid arthritis; platelet disorder;
XX thrombocytopaenia; aplastic anaemia; inflammatory disorder; septic shock;
XX systemic inflammatory response syndrome; SIRS; hormonal dysfunction;
XX cancer; atherosclerosis; wound; tissue regeneration; haemophilia;
XX leukaemia; reperfusion injury; psoriasis; diabetes; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 52..3996
XX /tag= a
XX /product= "GPCR #8"
XX /note= "This sequence is specifically claimed"
XX
PN WC200153454-A2.
XX
XX 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US034983.
XX
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 31-AUG-2000; 2000US-00653450.
XX 04-DEC-2000; 2000US-00729739.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Yamazaki V, Tang YT, Liu C, Zhou P, Wang D, Zhang J, Ren F;
XX Asundi V, Drmanac RT;
XX
XX WPI: 2001-442255/47.
XX P-PSDB; AAU04571.
XX
XX New G-protein-coupled receptor-like polypeptides and polynucleotides,
XX useful for treating diseases of ophthalmic, neurological, immunological
XX and nephritic systems and hormonal dysfunction, cancer, atherosclerosis
XX and diabetes.
XX
XX Claim 1; Page 197-202; 259pp; English.
XX
XX The sequence encodes a human G-protein coupled receptor (GPCR)-like
XX protein. The GPCR-like polypeptides and polynucleotides are useful for
XX the treatment of diseases of ophthalmic, neurological (e.g Alzheimer's
XX disease and Parkinson's disease, immunological (e.g HIV infection and
XX candidiasis), autoimmune disorders (e.g multiple sclerosis, systemic
XX lupus erythematosus and rheumatoid arthritis), platelet disorders (e.g
XX thrombocytopaenia and aplastic anaemia), inflammatory disorders (e.g.
XX septic shock and systemic inflammatory response syndrome, SIRS) and
XX nephritic systems. They may also be used to treat hormonal dysfunction,
XX cancer, atherosclerosis, wounds, tissue regeneration, haemophilia,
XX leukaemias, reperfusion injury, psoriasis and diabetes. Numerous examples
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QY	1 MetArgSerThrThrLeuLeuAlaLeuValLeuTyrLeuValSerGly 20
pb	1 ATGCAGACCAACGCTCCGGCCCCGTGGCGCTGGTTACTGGTGTCGTG 60





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Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 574 TGCTGTCTTGTTCCTCACGCCACGCTTCGTGTCTATATGAGGAGCTGGAGCAAG 633
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
Db 634 CTGGAGGCCATCTACTTGTTCATAGTACGCTTACCAACCGTGGGCTTTGGGCACTATGTG 693
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 694 GCCGGCGCGGACCCAGCAGGACTCCCGCGCTATCAGCGCTGTGTGTCTGGATC 753
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 754 CTGCTCGCGCTGGCTTACTTTCGCTCAGTGTCTACCACTCCGGAATCGCTCGAGTA 813
Qy 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 814 GTGTCCCGCGGCACTCGGCGAGAGTGGCGGCTTCAGGCTCAGGCTGCAGCTGGACT 873
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 874 GGCACAGTGACAGCGCGTGCACCGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGG 933
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 934 GAGCAGCACATG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 981
Qy 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340
Db 982 AGGCGCGCATCCCTTCGCGCCCGAGAGCTCGCGCGCTTCCCGCGCCAGCGCTCG 1041
Qy 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 1042 GCCCTGATTATCCAGCGAGAACCTGCGCTTCATCGACGAGTCTCGGATACGACAGC 1101
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
Db 1102 GAGCGCGGCTGCCGCTGCGCGCGCGCGCGCGAGAGTTCGCGCGCGCGCGCGCGCG 1161
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1162 AGCCCGGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1215
```

## RESULT 3

```
US-09-620-312D-195
; Sequence 195, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-09/552,317
; PRIOR FILING DATE: 2000-04-25
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; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 195
; LENGTH: 3996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3996)
US-09-620-312D-195
Alignment Scores:
Pred. No.: 2,83e-123 Length: 3996
Score: 1688.50 Matches: 327
Percent Similarity: 88.41% Conservative: 24
Best Local Similarity: 82.37% Mismatches: 41
Query Match: 81.22% Indels: 5
DB: 4 Gaps: 2
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US-09-655-272-2 (1-398) x US-09-620-312D-195 (1-3996)
Qy 1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuTyrLeuValSerGly 20
Db 1669 ATCGCAGACACACCGCTCTCGGCCCTGCTGGCGCTGTCTTGTCTTGTCTGTGT 1728
Qy 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40
Db 1729 GCCTCTGTGTTCGGGCGCTTGGAGAGCCCGCCAGCAGCAGCAGCAGCAGCAGCAG 1788
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 1789 GAGGTCCGAGAGAGTTCCTGAGGGCCCATCCGTGTGTGAGCAGCAGCAGCAGCAGC 1848
Qy 61 PheIleIysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 1849 CTCATCAAGAGAGTGTGCTGATGCCCTGGGAGGGGGTGGCGAGCCAGCAACCACTCG 1908
Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 1909 AGCAACAGACAGCAC---TCAGCTGGGACCTGGGAGCGGCTCTTTTCTCAGGAGCC 1965
Qy 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 1966 ATCATCACCACTCGCTATGGCAATGTGGCCCTGCGCACAGATGCGCGGCGCTCTTC 2025
Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 2026 TGCATCTTTATGCGCTGTGGGATTCGCTCTTTGGGATCTCTACTGGCAGGGGTGGG 2085
Qy 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 2086 GACCGCTGGGCTCTCCCTGCGCCATGGATCGATCGATCATGAGGCATCTTCTTGAAG 2145
Qy 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180
Db 2146 TGGCAGCTGCCACCGGAGCTAGTAAAGAGTGTCTGCGCGATGCTTTTCTCTGCTGATCG 2205
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 2206 TGCCTGCTCTCTTGTCTCAGCGCCACGTTCTGTCTATATGAGGAGCTCGAGCAAG 2265
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
Db 2266 CTGGAGGCCATCTACTTGTTCATAGTACGCTTACCAACCGTGGGCTTTGGGCACTATGTG 2325
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 2326 GCCGGCGCGGAGCCCGCAGGAGGACTCCCGCGCTATCAGCGCTGTGTGTGTCTGATC 2385
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
```

Thu Feb 3 07:31:01 2005

2386 CTGCTCGGCTGGCTTACTTGGCTCAGTGTCTACACACCATCGGAACCTGGCTGGAGTA 2445  
 261 ValSerArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 2446 GTGTCCGCGGCACTCGGCGAGAGATGGCGGCTCAGCGCTCAGGCTGCCAGCTGGACT 2505  
 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 2506 GGCACAGTGACAGCGGCGGTGACCCAGCAGCGCGGCGCGCGCGCGCGCGCGGAGAG 2565  
 301 GluGlnProLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320  
 2566 GAGCAGCCACTG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGGCTGGGC 2613  
 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 2614 AGCCCGCATCCCTTCGCGCCCGAGAGGCTCAGCGCTTCCCGCGCCAGCGCTCG 2673  
 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
 2674 GCCCTGATTTATCCAGCGAGAACCTGGCCCTTCATCAGCAGGTCCTCGGATACGACAGC 2733  
 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380  
 2734 GAGCGCGGCTGCCGCTGCCCGCGCGCGCGAGAGTCCGCGCGCCCAATCCCGCCAGG 2793  
 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValPro 397  
 2794 AAGCCCGTGGCG 2844

RESULT 4

US-09-799-451-432  
 ; Sequence 432, Application US/09799451  
 ; Patent No. 6783969  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Zhou, Ping  
 ; APPLICANT: Goodrich, Ryle  
 ; APPLICANT: Asundi, Vinod  
 ; APPLICANT: Ren, Feiyan  
 ; APPLICANT: Zhang, Jie  
 ; APPLICANT: Xue, Aidong J.  
 ; APPLICANT: Zhao, Qing A.  
 ; APPLICANT: Wang, Jian-Rui  
 ; APPLICANT: Ma, Junqing  
 ; APPLICANT: Yamazaki, Victoria  
 ; APPLICANT: Chen, Rui-hong  
 ; APPLICANT: Wang, Zhiwei  
 ; APPLICANT: Wang, Dunrui  
 ; APPLICANT: Yang, Yonghong  
 ; APPLICANT: Wehrman, Tom  
 ; APPLICANT: Ghosh, Reena  
 ; APPLICANT: Drmanac, Radoje T.  
 ; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
 ; TITLE OF INVENTION: Polypeptides  
 ; FILE REFERENCE: 803  
 ; CURRENT APPLICATION NUMBER: US/09/799,451  
 ; CURRENT FILING DATE: 2001-03-05  
 ; NUMBER OF SEQ ID NOS: 948  
 ; SOFTWARE: pt\_FL\_genes Version 2.0  
 ; SEQ ID NO 432  
 ; LENGTH: 2730  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (473) .. (2086)  
 ; US-09-799-451-432

Alignment Scores: 1.83e-54 Length: 2730  
 Pred. No.: 179  
 Score: 812.00 Matches:  
 Percent Similarity: 56.21% Conservative: 61

Best Local Similarity: 41.92% Mismatches: 132  
 Query Match: 39.06% Indels: 55  
 DB: 4 Gaps: 7  
 US-09-655-272-2 (1-398) x US-09-799-451-432 (1-2730)  
 QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuLeuValSerGly 20  
 DB 671 ATGAAGTGAAGACGGTGGTGGCATCTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 730  
 QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
 DB 731 GGTCTTCTTCGGGCACTTGGAGCAGCCCTTTGAGAGCAGCCAGAGATACCATCCGCC 790  
 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 DB 791 TTGAGAGGCGGGAATTCCTGGGGATCATGTCTGTGAGAGCCCGCAGGAGCTGGAGAG 850  
 QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThr 80  
 DB 851 TTGATCCAGCATGCTCTTGATGCTGACAATCGGGAGTCACTGCCA-----ATAGGA 901  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 DB 902 AACTCTTCCAAACACAGCAGCAGCCTGGGACCTCGGAGTGCCTTTTCTTGTGGAAC 961  
 QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 DB 962 GTCAATTACGACCATAGGTATGGGAATATTGCTCCGAGCACTGAAGAGGCAAAATCTTT 1021  
 QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
 DB 1022 TGTATTTTATATGTCATCTTTGGAAATCCACTCTTTGGTTCTTATTGGCTGGAATTGA 1081  
 QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 DB 1082 GACCAACTTGGACCATCTTTGGGAAAGCATTCGACAGTGGAGAGGTCTTTCGAAAA 1141  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuLeuPheLeuLeuIleGly 180  
 DB 1142 AAGCAAGTGAGTCAGACCAAGATCCGGGTCTATCAACCATCTCTGTTCTATCTTGGCGGC 1201  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
 DB 1202 TGCATTGTGTTTGTGACGATCCCTGCTGCTCATCTTTAAGTATCATCGAGGCTGGACGCC 1261  
 QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220  
 DB 1262 TTGGAGTCCATTTACTTTGTGGTGTCTCTGACCCCGGTGGGCTTTGGTGAITTTGTG 1321  
 QY 221 ProGlyAspGlyThrGlyGlnAsn---SerProAlaTyrGlnProLeuValTrpPheTrp 239  
 DB 1322 GCAGGGGAAACGCTGGCATCAATATTATCGGGAGTGGTATAGCCCTAGTGTGGTTTGG 1381  
 QY 240 IleLeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArg 259  
 DB 1382 ATCTTTGTGGCTTGCCTTACTTTGAGCTGCTCTCAGTATCATCGGAGATTGGGTACGG 1441  
 QY 260 AlaValSerArgArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTrp 279  
 DB 1442 GTTCTGTCCAAAAGACAAAGAGAGGTGGGTGAATCAAGGCCCATCGGCAGAGTGG 1501  
 QY 280 ThrGlyThrValThrAlaArgVal----- 287  
 DB 1502 AAGCCCAATGTCACTGCTGAGTTCGGGAGACACGCGGAAGGCTCAGCGTGGAGATCCAC 1561  
 QY 288 -----ThrGlnArgThrGly-ProSerAlaPro----- 296  
 DB 1562 GATAAGCTGACGCGCGCGCCACCATCCGCGCAGCATGGAGCGCGCGGCTGGCGCTGGAC 1621  
 QY 297 -----ProProGluLysGluGlnProLeuLeuProse 307  
 DB 1622 CAGCGGGCCCACTCACTGGACATGCTGCTCCCGGAGAGCGCTCTGCTTTTGTGCGCTG 1681

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QY 307 rSerLeuProAlaProProAlaValValGluProAlaGlyArgProGlySerProAlaPr 327
DB 1682 GACA-----CCGCCCGCTTCAAGAGCTCATCCAGG----- 1712

QY 327 oAlaGluLysValGluThrProSerProProAlaSerAlaLeuAspTyrProSerGl 347
DB 1713 -----AGAGCATCAACAACCGGCCCAACACCTCGCCCTGAAGGGCCGGAGCAGCTG 1765

QY 347 uAsnLeuAlaPheIleAspGluSerSerAspThrGlnSerGluArgGlyCysAlaLeuPr 367
DB 1766 AACAGCATCGGCGAGGTGGTCCGAGGACAAACATCATCAACAGTTCCGGTCCACCTCC 1825

QY 367 oArgAlaProArgGlyArgArg-----ProAsnProSerLysLys 381
DB 1826 AGACTCACCAAGAGGAAAAACAAGGACCTCAAAAAGACCTTGCCCGAGGAGCGTTTCAGAA 1885

QY 381 sProSerArgProArgGly 387
DB 1886 ATCTACAAGACCTTCGCGA 1904

RESULT 5
US-09-236-080-5
; Sequence 5, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25,
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-236-080-5

Alignment Scores:
Pred. No.: 1,88e-52 Length: 1994
Score: 784.00 Matches: 161
Percent Similarity: 62.04% Conservative: 58
Best Local Similarity: 45.61% Mismatches: 111
Query Match: 37.71% Indels: 23
DB: 3 Gaps: 3

US-09-655-272-2 (1-398) x US-09-236-080-5 (1-1994)

QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuTyrLeuValSerGly 20
DB 607 ATGAATGGAAGACAGTCTCCACGATTTTCTGGTGTCTCTCTACCTGATCATCGGA 666

QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40
DB 667 GCCCGCGTGTTCAGGCAATTCAGGACCTTCAGGACATTTCCCGAGAGACCACTTTGTG 726

QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
DB 727 ATCCAGAGCAGACCTTCATAGCCCGACGCTGCGTCAACTCCACCGAGCTGGACGAA 786

QY 61 PheIleLeuLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThr 80
DB 787 CTATCCAGCAATAGTGGCAGCAATAAAGCGGGATTATCCCT-----TTAGGA 837

QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
DB 838 AACAGCTCCAATCAAGTTAGTCACTGGGACCTCGAAGCTCTTCTCTTTGCTGTACT 897

QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
DB 898 GTTATCAACCACTAGGATTTGGAAACATCTCCCAACGAACATCTCCCAAGGTGGAATAATTC 957
```

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QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
DB 958 TGCATCATCTATGCTTGTGGGAATTCCTCTTTGGCTTTCTACTGGCTGGGTGGT 1017

QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 1018 GATCAGCTAGGAACATATATTGGAAAGGAATTTGCCAAATGGAGACACATTTATTAA 1077

QY 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180
DB 1078 TGGATGTTAGTCAGAGGAAGATTCTATCATCTCCACCATCATCTTCCTCTTTGGC 1137

QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
DB 1138 TGTGTCTCTTGTGGCTCTCCCTCGGTGCATATTCAAGCACATAGAAGCTGGAGCGCC 1197

QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
DB 1198 CTGGAGCGCTATCTATTTTGTGTATCTACTGACGACCATTTGGATTTGGAGACTACGTG 1257

QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
DB 1258 GCAGGTGGATCAGACATTCGACTTCTACAGCTGTGTGTGTCTGATC 1317

QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
DB 1318 CTCTGTGGCTGCGCTTACTTTCAGCTGTCTGAGCATGATTGGGACTGGCTACGGTG 1377

QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
DB 1378 ATCTCTAAGAACGAGGAAGAGGTGGGAGAGTTCCAGAGCGCATCCCTGAGTGACA 1437

QY 281 GlyThrValThrAlaArgValThrGln-Arg-----Th 291
DB 1438 GCCAATGTCACGCGCAGTTCAGGAAACGAGGAGCGGCTGAGCGTGAGATCTACGAC 1497

QY 291 rGlyProSerAlaProProProGluLysGluGlnProLeuLeuProSerSerLeuProA 311
DB 1498 AAGTTCAGCGTGGCCACATCCGTGAAGCGAAGCTCTCCGACAGAGCTGGCGGCAACCAC 1557

QY 311 laPro-----ProAlaValGluProAlaGlyArgProG 323
DB 1558 AACACGAGAACTGACTCCGTGTATGAGGACCTCTGTGTGAACCATCTGACCGAGAGG 1617

QY 323 lysSerProAla-ProAlaGluLysValGluThr 333
DB 1618 GAAGTCTGCTCCCTTCTGCTGAGGCTGAGAC 1650

RESULT 6
US-09-236-080-1
; Sequence 1, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1246
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-236-080-1

Alignment Scores:
Pred. No.: 2,86e-52 Length: 1246
Score: 778.00 Matches: 149
Percent Similarity: 67.53% Conservative: 59
Best Local Similarity: 48.38% Mismatches: 87
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## RESULT 7

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Qy   181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerIlys 200
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
704 TGTCTACTCTTTTGTCCTCCCTCGCATCATATTAACAACATAGAGGGCTGGAGTGCC 763
Qy   201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
764 CTGACGCCATTATTTTGTGGTATTCACTCTAACAATATGTGATTTGGTAGCTACGTT 823
Qy   221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
824 GCAGGTGGATCCGATATTGAATATCTGGACTCTTATAAGCCTCGTCTGCTCTGGATC 883
Qy   241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
884 CTTGTAGCGGCTTGCTTACTTTGCTGCTCTGAGCATGATTGGAGATTGGCTCCGAGTG 943
Qy   261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAsaSerTrpThr 280
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
944 ATATCTAAAGAAGACAAAGAAGAGGTGGAGAGTTTCAGAGCACACGCTGCTGAGTGGACA 1003
Qy   281 GlyThrValThrAla-----ArgValThrGlnArg-----Th 291
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
1004 GCCAACGTCACAGCGCGAATTCCAAGAAACCAGGAGGCGAGCTGAGTGTGAGATTATGAC 1063
Qy   291 rGlyProSerAlaProProPro 298
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
1064 AAGTTCACAGCGGCACCTCCA 1085

RESULT 8
US-09-561-763-3
; Sequence 3, Application US/09561763
; Patent No. 6664373
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: WNI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1497)
US-09-561-763-3

Alignment Scores:
Pred. No.:      2,25e-25      Length:      1497
Score:          438.00        Matches:     130
Percent Similarity: 43.51%    Conservative: 78
Best Local Similarity: 27.20% Mismatches:     144
Query Match:     21.07%      Indels:      127
DB:              4           Gaps:         16

US-09-655-272-2 (1-398) x US-09-561-763-3 (1-1497)

Qy   9 LeuLeuAlaLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPheGlnAlaIeuGlu 28
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
22 CTCACCTTGGCCATCATCTTCTACTTGGCCATCGGGGGCGCATCTTCGAAGTCTGGAG 81
Qy   29 GlnProHisGluGlnGlnAlaGlnLysLysMetAspHisGlyArgAspGlnPheLeuArg 48
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
82 GAGCCACACTGGAAGGAGGCCAAGAAAACTACTACACAGAGAGCTGCATCTGCTCAAG 141
Qy   49 AspHisProCysValSerGlnLysSerLysLeuAspPheIleLysLeuLeuValGluAla 68
Db       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

```

QY 341 -AlaLeuAspTyr-----ProSerGluAsnLeuAlaPheIleAspGluSe 355  
 Db 1218 CGCCAGGAGTACACCCACTCATCTTCAGGAGCGCCAGCATCACCTTCGTGAACGGA 1277  
 QY 355 rSerAsp-ThrGlnSerGluArgGlyCysAlaLeuProArgAlaProArg----- 371  
 Db 1278 GGCTGGCTCTCAGACGAGAGA-----CCTCAAGTCTCTCGCTAGAGGACAA 1325  
 QY 372 -----GlyArgArgProAsnProSerLysLysProSerArgPro 385  
 Db 1326 CTTGGCAGGGAGGAGAGCCCGCAGCAGGGGGCTGAAGCCAGGCGCCCC 1375  
 RESULT 9  
 US-09-431-367B-3  
 ; Sequence 3, Application US/09431367B  
 ; Patent No. 6670149  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Rory A.J.  
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MNI-074CP  
 ; CURRENT APPLICATION NUMBER: US/09/431.367B  
 ; CURRENT FILING DATE: 1999-11-01  
 ; PRIOR APPLICATION NUMBER: 09/259,951  
 ; PRIOR FILING DATE: 1999-03-01  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1497  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1497)  
 US-09-431-367B-3  
 Alignment Scores:  
 Pred. No.: 2,258-25 Length: 1497  
 Score: 438.00 Matches: 130  
 Percent Similarity: 43.51% Conservative: 78  
 Best Local Similarity: 27.20% Mismatches: 144  
 Query Match: 21.07% Indels: 127  
 DB: 4 Gaps: 16  
 US-09-655-272-2 (1-398) x US-09-431-367B-3 (1-1497)  
 QY 9 LeuLeuAlaLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPheGlnAlaLeuGlu 28  
 Db 22 CTCACCTCGGCATCATCTTCTACCTGGCCATCGGGCGCGGATCTTCGAAGTGTGGAG 81  
 QY 29 GlnProHisGluGlnGlnAlaGlnLysLysMetAspHisGlyArgAspGlnPheLeuArg 48  
 Db 82 GAGCCACACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 141  
 QY 49 AspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeuValGluAla 68  
 Db 142 GAGTTCGGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 201  
 QY 69 LeuGlyGlyGlyAlaAsnProGluThrSerTyrThrAsnSerSerAsnHisSerAla 88  
 Db 202 GCAGGACAGGGT-----GTGGCCATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246  
 QY 89 TrpAsnLeuGlySerAlaPhePheSerGlyThrIleIleThrThrIleGlyTyrGly 108  
 Db 247 TGAACCTGGCCCAATGCAATGATTTTGCAGGACCGCTCATACCATTCATGATGATGATG 306  
 QY 109 AsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheThrAlaLeuValGly 128  
 Db 307 AATGTGGCTCCCAAGACCCCGCGGTGGCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 366  
 QY 129 IleProLeu-----PheGlyMetLeuLeuAlaGlyValGlyAsp 141  
 Db 367 GTGCCGCTCTGCTGACGTGATCAGTGGCCCTGGGCAAGTCTTCGGGGGAGCGTCCCAAG 426

QY 142 ArgLeuGlySerSerLeu---ArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 Db 427 AGACTAGGAGGAGTTCCTTACCAAGAGAGGTGTGAGTCTGCGAAGGCG----- 474  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180  
 Db 475 -----CAGATCAGCTGACAGTCACTTCATCTGTCGTGGGCG 510  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTyrSerLys 200  
 Db 511 GTCCTAGTCCACCTGGTGATCCACCTTCGTATTCATGGTGACTGAGGGGTGGAATC 570  
 QY 201 LeuGluAlaIleTyrPheValIleValThrThrThrValGlyPheGlyAspTyrVal 220  
 Db 571 ATCAGGAGGCTCTACTACTCTTCATCACCATCCACCATCGCTTCGCTGACTTTGTG 630  
 QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAla---TyrGlnProLeuValTyrPheTyr 239  
 Db 631 GCCGGTGTGAACCCCGAGCGCCACTACCGCCCTGTACCGCTACTTCGTGGAGCTCTGG 690  
 QY 240 IleLeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTyrLeu--- 258  
 Db 691 ATCTACTTGGGGCTGGCTGG-----CTGTCCCTTTTGTCAACTGGAAGGTG 738  
 QY 259 -----ArgAlaValSerArgThrArgAla----- 267  
 Db 739 AGCATGTTTGTGAAGTCCACAAAGCCATTAAAGAGCGCGCGCGCCGACGGAAGGATCC 798  
 QY 268 ---GluMetGlyGlyLeuThrAlaGlnAlaAlaSerTyrThrGlyThrValThrAla--- 285  
 Db 799 TTTGAGAGCTCCACACTCCGGAGGCCCTGCGAGGTGAAGGGGAGCAGACGCTCCAAG 858  
 QY 285 ----- 285  
 Db 859 GACGTCAACATCTTCAGCTTTCTTCAAGAGGAGAGACCTACAACGACTCATCAAG 918  
 QY 286 -----ArgValThrGlnArgThr-----GlyProSer 294  
 Db 919 CAGATCGGGAAGAGCCCATGAAGACAAGCGGGGTGGGAGACGGGCCCGGCCAGGG 978  
 QY 295 AlaProProGlyLysGlnGlnProLeuLeuProSerSerLeuProAlaProAla 314  
 Db 979 CTGGGGCTCAAGCGGTGGCTCCAGCAGCTGCCCCCTTCCCTGGT-GCCCCCTGGTAGT 1037  
 QY 315 ValValGluProAlaGly-----Arg 321  
 Db 1038 CTACTCCAAGAACCGGGTGGCCCTTGAAGAGGTGTCAAGACACTGAGGAGCAAGG 1097  
 QY 322 ProGly-SerProAlaProAlaGlyLysValGluThrProSerProProThrAlaSer-- 340  
 Db 1098 CCACGTATCAAGTCCCGAGTGAAGAGGCTGTGGCAGCGGCCCTGGAAGACAGCTCCCC 1157  
 QY 340 ----- 340  
 Db 1158 TGCCCCGAGGTGTTTCATGAACAGCTGGACCGCATCAGCGAGGAATGCGACCATGGA 1217  
 QY 341 -AlaLeuAspTyr-----ProSerGluAsnLeuAlaPheIleAspGluSe 355  
 Db 1218 CGCCAGGAGTACACCCACTCATCTTCAGGAGCGCCAGCATCACCTTCGTGAACGGA 1277  
 QY 355 rSerAsp-ThrGlnSerGluArgGlyCysAlaLeuProArgAlaProArg----- 371  
 Db 1278 GGCTGGCTCTCAGACGAGGAGA-----CCTCAAGTCTCTCGCTAGAGGACAA 1325  
 QY 372 -----GlyArgArgProAsnProSerLysLysProSerArgPro 385  
 Db 1326 CTTGGCAGGGAGGAGAGCCCGCAGCAGGGGGCTGAAGCCAGGCGCCCC 1375

RESULT 10  
 US-09-561-763-1  
 ; Sequence 1, Application US/09561763  
 ; Patent No. 6664373



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; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(1506)
; US-09-561-763-1

Alignment Scores:
Pred. No.: 7,39e-25 Length: 3452
Score: 438.00 Matches: 130
Percent Similarity: 43.51% Conservative: 78
Best Local Similarity: 27.20% Mismatches: 144
Query Match: 21.07% Indels: 127
DB: 4 Gaps: 16

US-09-655-272-2 (1-398) x US-09-561-763-1 (1-3452)

QY 9 LeuLeuAlaLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPheGlnAlaLeuGlu 28
DB 31 CTCACCTCGGCCATCATCTTCTACCTGGCCATCGGGCGCGCATCTTCGAAGTCTGGAG 90
QY 29 GlnProHisGluGlnGlnAlaGlnLysLysMetAspHisGlyArgAspGlnPheLeuArg 48
DB 91 GAGCCACACTGGAAGGAGGAGGCAAGAACTACTACACACAGAGGCTGCTCAAG 150
QY 49 AspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeuValGluAla 68
DB 151 GAGTTCCTCGGCTGGGTGAGGAGGCTGACAGATCTTAGAGTGGTATCTGATGCT 210
QY 69 LeuGlyGlyAlaAsnProGluThrSerTrpThrAsnSerSerAsnHisSerSerAla 88
DB 211 GCAGGACAGGCT-----GTGGCCATCACAGGGAACAGACCTTCAACAAC--- 255
QY 89 TrpAsnLeuGlySerAlaPhePheSerGlyThrIleIleThrIleGlyTyrGly 108
DB 256 TGGAACTGGGCCAATGCAATGATTTTTCAGCGACCGCTCATACCACTTGGATATGGC 315
QY 109 AsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyrAlaLeuValGly 128
DB 316 AATGTGGCTCCCAAGACCCCGCGGTGGCTCTTCTGTGTTCATGTCTCTTCGGG 375
QY 129 IleProLeu-----PheGlyMetLeuLeuAlaGlyValGlyAsp 141
DB 376 GTGCGCTCTGCTGACGTGATCAGTCCCTGGCAAGTCTTCGGGGGACGTGCCAAG 435
QY 142 ArgLeuGlySerSerLeu---ArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 436 AGACTAGGCGAGTTCCTTACCAAGAGAGGTGTAGTCTGCGGAAGGCG----- 483
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180
DB 484 -----CAGATCAGCTGCACAGTCATCTTCATCGTGTGGGG 519
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
DB 520 GTCTAGTCCACCTGGTGATCCCACTTCTGATTCATGTGCTGAGGGTGAACATAC 579
QY 201 LeuGluAlaIleTyrPheValIleValLeuThrThrValGlyPheGlyAspTyrVal 220
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DB 580 ATCGAGGGCTCTACTACTCTTCTTCCATCACCATCTCCACCATCGGCTTCGGTGACTTTGTG 639
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAla---TyrGlnProLeuValTrpPheTrp 239
DB 640 GCGGGTGTGAACCCCGACGCGCAACTACCACGCGCTGTACGCTACTTCGTGGAGCTCTGG 699
QY 240 IleLeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeu--- 258
DB 700 ATCTACTTGGGGTGGCTGG---CTGTCCCTTTTGTCACTGGAAGGTG 747
QY 259 -----ArgAlaValSerArgArgThrArgAla----- 267
DB 748 AGCATGTTTGTGAAGTCCACAAGCCATTAGAAGCGCGCGCGGCGGAGGAGTCC 807
QY 268 ---GluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThrGlyThrValThrAla--- 285
DB 808 TTTGAGAGCTCCCACTCCCGGAAGGCCCTGCAGGTGAAGGGGAGCACAGCTCCAAG 867
QY 285 ----- 285
DB 868 GACGTCAACATCTTCAGCTTTCTTCCAAGAAGAGAGACCTTACAACGACCTCATCAAG 927
QY 286 -----ArgValThrGlnArgThr-----GlyProSer 294
DB 928 CAGATCGGAAGAGAGCCATGAAGACAGCGGGGTGGGAGACGGGCCCGGCGCCAGGG 987
QY 295 AlaProProGluLysGluGlnProLeuLeuProSerSerLeuProAlaProAla 314
DB 988 CTGGGCGCTCAAGGCGGTGGCTCCCGACGACTGCCCCCTTCCCTGCT-GCCCCCTGTGTAGT 1046
QY 315 ValValGluProAlaGly-----Arg 321
DB 1047 CTACTCCAAGAACCGGTGCCACCTTGAAGAGGTGTACAGACACTGAGGAGCAAGG 1106
QY 322 ProGly-SerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer-- 340
DB 1107 CCAGTATCAAGTCCCCAGATGAGGAGGCTGTGGCAGCGGCCCTGAAGACAGCTCCCC 1166
QY 340 ----- 340
DB 1167 TGCCCCGAGGTGTTTCATGAACGACGCTGGACCGCATCAGCGAGGAATCGAGCCATGGGA 1226
QY 341 -AlaLeuAspTyr-----ProSerGluAsnLeuAlaPheIleAspGluSe 355
DB 1227 CGCCAGGACTACCACTTCCAGGACGCGCATCACCTTCGTGAACACGGA 1286
QY 355 rSerAsp-ThrGlnSerGluArgGlyCysAlaLeuProArgAlaProArg----- 371
DB 1287 GGCTGGCTCTCAGACGAGAGA-----CCTCAAGTCTTCGTAGAGGACAA 1334
QY 372 -----GlyArgArgArgProAsnProSerLysLysProSerArgPro 385
DB 1335 CTGGCAGGGGAGGAGAGCGCCCGACGAGGGGCTGAAGCCAGCGGCC 1384
RESULT 11
US-09-431-367B-1
; Sequence 1, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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**ug-09-655-272-2.rni**

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928	Db	CAGATCGGGAGGAAGGCATATGAACA	CAACGGGGGGTGGGACACGGGCCCGGCCG	CGG	987
295	QY	AlaProProGluLysGluGlnProLeuLeuProSerSerLeuProAlaProProIla			314
988	Db	CTGGGGGCTCAAGCGCGTGGGTCTCCAGACATCGCCCTTCCCTCGT	GCCTCTGGTATG	1046	

---Arg 321

Db	1047	CTACTCCAAGAAACGGGTGCCACCTTGAAGAGGTGTACAGACACTGAGGAGCAAAAGG	1106
Qy	322	ProGly-SerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer--	340
Db	1107	CCACGTATCAAGTCTCCACATGAGGAGGCTGTGGCAGCGGCCCTTGAAGACAGCTCCCC	1166
Qy	340	-----	340
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Qy	341	-AlaLeuAspTyr-----ProSerGluAsnLeuAlaPheIleAspGluSe	355
Db	1227	CGCCCGAGCACTACCAACCACTCATCTTCAGGAGCGGCAGCATCACCTTGTGAACACGGA	1288
Qy	355	-SerAsp-ThrGlnSerGluArgGlyCysAlaLeuProArgAlaProArg-----	371
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Qy	372	-----GlyArgArgArgProAsnProSerLysLysProSerArgPro	385
Db	1335	CTTGGCAGGGAGGAGAGCCCCCAGCAGGGGGGTGAAGGCCAGGCGCCCC	1384
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; Sequence 6, Application US/09561763			
; Patent No. 6664373			
; GENERAL INFORMATION:			
; APPLICANT: CURTIS, ROY A.J. ET AL.			
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR			
; FILE REFERENCE: MNI-074CP2			
; CURRENT APPLICATION NUMBER: US/09/561,763			
; CURRENT FILING DATE: 2000-04-29			
; PRIOR APPLICATION NUMBER: 09/431,367			
; PRIOR FILING DATE: 01-11-1999			
; PRIOR APPLICATION NUMBER: US 09/259,951			
; PRIOR FILING DATE: 01-03-1999			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: Patent in ver. 2.0			
; SEQ ID NO 6			
; LENGTH: 996			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(996)			
US-09-561-763-6			
Alignment Scores:			
Pred. No.: 8,48e-25 Length: 996			
Score: 427.50 Matches: 111			
Percent Similarity: 51.79% Conservative: 48			
Best Local Similarity: 36.16% Mismatches: 115			
Query Match: 20.56% Indels: 33			
DB: 4 Gaps: 8			
US-09-655-272-2 (1-398) x US-09-561-763-6 (1-996)			
Qy	5	ThrLeuLeuAlaLeuAlaLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPhe	24

Alignment Scores:	8.48e-25	Length:	996
Pred. No.:	427.50	Matches:	111
Score:	51.79%	Conservative:	48
Percent Similarity:	36.16%	Mismatches:	115
Best Local Similarity:	20.56%	Indels:	33
Query Match:	4	Gaps:	8

772 00 055 033-3 (1-200) x 118-09-561-763-6 (1-996)

5 ThrLeuLeuAlaLeuLeuAlaLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPhe 24

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Db 64 ACCGTGCTCTGCTGCTGCGC---TACCTGGCTTACCTGGCGTGGCCACCGCGGTGTTTC 120
Qy 25 GlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAspHisGlyArgAsp 44
Db 121 TGGACGCTGGAGGCGCGCGCGCGAGGACTCCAGCGCGAGCTTCAGCGCGCAAGTGG 180
Qy 45 GlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeu 64
Db 181 GAGCTGTGCAAGAACTTCACTGCTCGACCGCGCGCGCTGAGCTCGCTGATCCGGAT 240
Qy 65 LeuValGluAlaLeuGlyGlyAlaAenProGluThrSerTrpThrAsnSerAsn 84
Db 241 GTCGTCCAGCATACAAAACGAGGC-----AGCCTCTCCAGCAACACACC 288
Qy 85 HisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIleThrThr 104
Db 289 AGCATGGGCGCTGGAGCTCGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 348
Qy 105 IleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyr 124
Db 349 ATTGGCTATGGCAACCTGAGTGTGTGACCAACATGCTGCTGCTGCTGCTGCTGCT 408
Qy 125 AlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGlyAspArgLeuGly 144
Db 409 GCCCTTGTGGGATCCCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 456
Qy 145 SerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLysTrpHisValPro 164
Db 457 CATCTCATGACGAGGAGTAACCACTGGCGCCAGCAGGCTGGGGGCGACCTGGCAGGAT 516
Qy 165 ProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGlyCysLeuPhe 184
Db 517 CCTGCAAGGCGCGGTGGTGGCGGCTCTGGCGGCTCTGGCGGCTCTCTCTCTCTCTCT 576
Qy 185 ValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLysLeuGluAlaIle 204
Db 577 CTGCTGCTCCACCGCTGCTCTCTCTCCCATGGAGGCTGGAGCTTACACAGAGGGCTTC 636
Qy 205 TyrPheValIleValThrLeuThrValGlyPheGlyAspTyrValProGlyArgGly 224
Db 637 TACTTGGCTTCTATCACTCCCTGAGCCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 696
Qy 225 ThrGlyGlnAsnSerProAla---TyrGlnProLeuValTrpPheTrpIleLeuPheGly 243
Db 697 CCTCCACAGAGGTACCCACTGTGTGTACAAAGAACATGCTGCTGCTGCTGCTGCTGCT 756
Qy 244 LeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArg 263
Db 757 ATGGCATGGCTGGCTGTGATCACTCAAACTCACTCACTCACTCACTCACTCACTCACT 816
Qy 264 -----ArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAla 276
Db 817 GTATGCTCTGTCGCCACCACTCTAGGAAGACTTC-----AGTCC 861
Qy 277 AlaSerTrpThrGlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaPro 296
Db 862 CAAAGCTGG-----AGACAGGAGGACCTGACCGG--- 888
Qy 297 ProProGluLysGluGlnPro 303
Db 889 GAGCCAGAGTCCCACTCCCA 909
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## RESULT 13

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US-09-431-367B-6
; Sequence 6, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MXI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
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; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
; US-09-431-367B-6

Alignment Scores:      8.48e-25      Length:      996
Pred. No.:            427.50          Matches:     111
Score:                51.79%          Conservative: 48
Percent Similarity:   36.16%          Mismatches:  115
Best Local Similarity: 20.56%          Indels:      33
Query Match:          4               Gaps:        8
DB:

US-09-655-272-2 (1-398) x US-09-431-367B-6 (1-996)
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Qy 5 ThrLeuLeuAlaLeuLeuAlaLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPhe 24
Db 64 ACCGTGCTCTGCTGCTGCTGCGC---TACCTGGCTTACCTGGCGTGGCCACCGCGGTGTTTC 120
Qy 25 GlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAspHisGlyArgAsp 44
Db 121 TGGACGCTGGAGGCGCGCGCGCGAGGACTCCAGCGCGAGCTTCAGCGCGCAAGTGG 180
Qy 45 GlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeu 64
Db 181 GAGCTGTGCAAGAACTTCACTGCTCGACCGCGCGCGCTGAGCTCGCTGATCCGGAT 240
Qy 65 LeuValGluAlaLeuGlyGlyAlaAenProGluThrSerTrpThrAsnSerAsn 84
Db 241 GTCGTCCAGCATACAAAACGAGGC-----AGCCTCTCCAGCAACACACC 288
Qy 85 HisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIleThrThr 104
Db 289 AGCATGGGCGCTGGAGCTCGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 348
Qy 105 IleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyr 124
Db 349 ATTGGCTATGGCAACCTGAGTGTGTGACCAACATGCTGCTGCTGCTGCTGCTGCT 408
Qy 125 AlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGlyAspArgLeuGly 144
Db 409 GCCCTTGTGGGATCCCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 456
Qy 145 SerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLysTrpHisValPro 164
Db 457 CATCTCATGACGAGGAGTAACCACTGGCGCCAGCAGGCTGGGGGCGACCTGGCAGGAT 516
Qy 165 ProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGlyCysLeuPhe 184
Db 517 CCTGCAAGGCGCGGTGGTGGCGGCTCTGGCGGCTCTGGCGGCTCTCTCTCTCTCTCT 576
Qy 185 ValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLysLeuGluAlaIle 204
Db 577 CTGCTGCTCCACCGCTGCTCTCTCTCCCATGGAGGCTGGAGCTTACACAGAGGGCTTC 636
Qy 205 TyrPheValIleValThrLeuThrValGlyPheGlyAspTyrValProGlyArgGly 224
Db 637 TACTTGGCTTCTATCACTCCCTGAGCCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 696
Qy 225 ThrGlyGlnAsnSerProAla---TyrGlnProLeuValTrpPheTrpIleLeuPheGly 243
Db 697 CCTCCACAGAGGTACCCACTGTGTGTACAAAGAACATGCTGCTGCTGCTGCTGCTGCT 756
Qy 244 LeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArg 263
Db 757 ATGGCATGGCTGGCTGTGATCACTCAAACTCACTCACTCACTCACTCACTCACTCACT 816
Qy 264 -----ArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAla 276
Db 817 GTATGCTCTGTCGCCACCACTCTAGGAAGACTTC-----AGTCC 861
Qy 277 AlaSerTrpThrGlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaPro 296
Db 862 CAAAGCTGG-----AGACAGGAGGACCTGACCGG--- 888
Qy 297 ProProGluLysGluGlnPro 303
Db 889 GAGCCAGAGTCCCACTCCCA 909
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Db 757 ATGGCATGCTGGCTTGTATCATCAAACTCATCTCCAGCTGGAGACGCCAGGAGG 816  
 Qy 264 -----ArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAla 276  
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 Qy 277 AlaSerTrpThrGlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaPro 296  
 Db 862 CAAAGCTGG-----AGACAGGAGCCTGACCGG--- 888  
 Qy 297 ProProGluLysGluGlnPro 303  
 Db 889 GAGCCAGAGTCCCACTCCCA 909

RESULT 14  
 US-09-561-763-4  
 ; Sequence 4, Application US/09561763  
 ; Patent No. 6664373  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Rory A.J. et al.  
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MNI-074CP2  
 ; CURRENT APPLICATION NUMBER: US/09/561,763  
 ; CURRENT FILING DATE: 2000-04-29  
 ; PRIOR FILING DATE: 01-11-1999  
 ; PRIOR APPLICATION NUMBER: US 09/259,951  
 ; PRIOR FILING DATE: 01-03-1999  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (122)..(1117)  
 US-09-561-763-4

Alignment Scores: 1.63e-24 Length: 1575  
 Pred. No.: 427.50 Matches: 111  
 Percent Similarity: 51.79% Conservative: 48  
 Best Local Similarity: 36.16% Mismatches: 115  
 Query Match: 20.56% Indels: 33  
 DB: 4 Gaps: 8  
 US-09-655-272-2 (1-398) x US-09-561-763-4 (1-1575)  
 Qy 5 ThrLeuLeuAlaLeuAlaLeuValLeuLeuValSerGlyAlaLeuValPhe 24  
 Db 185 ACCGTGCTCTCTCTCTGCCC---TACCTGGCTTACCTGGCGTGGCCACCGCGTGTTC 241  
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 Qy 45 GlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeu 64  
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 Db 470 ATTGGCTATGGCAACCTGAGCCCCACACAGATGGCTGCGCGCTCTCTCTGATCTCTTT 529

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RESULT 15  
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 ; Sequence 4, Application US/09431367B  
 ; Patent No. 6670149  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Rory A.J.  
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MNI-074CP  
 ; CURRENT APPLICATION NUMBER: US/09/431,367B  
 ; CURRENT FILING DATE: 1999-11-01  
 ; PRIOR APPLICATION NUMBER: 09/259,951  
 ; PRIOR FILING DATE: 1999-03-01  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1575  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (122)..(1117)  
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 DB: 4 Gaps: 8  
 US-09-655-272-2 (1-398) x US-09-431-367B-4 (1-1575)



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GenCore version 5.1.6  
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Run on: February 3, 2005, 01:34:36 ; Search time 697.536 Seconds  
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Title: US-09-655-272-2

Perfect score: 2079

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Total number of hits satisfying chosen parameters: 8600550

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1692.5	81.4	1257	9	US-09-828-035-3
3	1692.5	81.4	1257	15	US-10-146-733-30
4	1692.5	81.4	1260	15	US-10-345-680-45
5	1692.5	81.4	1260	15	US-10-391-399-20
6	1692.5	81.4	1408	9	US-09-828-035-1
7	1692.5	81.4	1408	15	US-10-146-733-28
8	1692.5	81.4	1408	15	US-10-352-684A-7
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10	1692.5	81.4	2747	18	US-10-768-158-11
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19	812	39.1	1614	11	US-09-892-360-1
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43	490.5	23.6	1009	18	US-10-343-903-38
44	490	23.6	882	13	US-10-121-966-3
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ALIGNMENTS

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; Sequence 1, Application US/10243035  
; Publication No. US20030049697A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZDUNSKI, MICHEL  
; APPLICANT: LESAGE, FLORIAN  
; APPLICANT: MAINGRET, FRANCOIS  
; TITLE OF INVENTION: NEW FAMILY OF MECHANOSENSITIVE HUMAN POTASSIUM CHANNELS  
; FILE REFERENCE: 1317-02  
; CURRENT FILING DATE: 2002-09-13  
; CURRENT APPLICATION NUMBER: US/10/243,035  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1182  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS



LOCATION: (1)..(1179)  
US-10-243-035-1

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Pred. No.: 3 24e-142 Length: 1182  
Score: 1692.50 Matches: 328  
Percent Similarity: 88.44% Conservatives: 24  
Best Local Similarity: 82.41% Mismatches: 41  
Query Match: 81.41% Indels: 5  
DB: 14 Gaps: 2

US-09-655-272-2 (1-398) x US-10-243-035-1 (1-1182)

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QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
DB 61 GCCCTGGTGTTCGGGCCCTGGAGCAGCCCAACGAGCAGCGCCAGAGGAGCTGGG 120

QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
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QY 61 PheileLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
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QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
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Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
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Qy 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaSerTrpThr 280
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; Publication No. US20030219806A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Lora, Jose M.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: NOVEL 18607, 15603, 69318, 12303, 48000,
; TITLE OF INVENTION: 52920, 5433, 38554, 57301, 58324, 55063, 52991, 59914, 59921
; TITLE OF INVENTION: AND 33751 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MP103-0200NM
; CURRENT APPLICATION NUMBER: US/10/391.399
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; PRIOR APPLICATION NUMBER: US 09/789,481
; PRIOR FILING DATE: 2001-02-20
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; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 09/583,373
; PRIOR FILING DATE: 2000-05-31
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; PRIOR FILING DATE: 2000-02-22
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; PRIOR FILING DATE: 2002-12-04
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; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US60/275,078
; PRIOR FILING DATE: 2001-03-12
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; PRIOR FILING DATE: 2001-04-06
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; PRIOR FILING DATE: 2000-04-07
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; SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 1260
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; FEATURE:
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; LOCATION: (1)...(1260)
; US-10-391-399-20

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Score: 1692.50 Matches: 328
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Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 15 Gaps: 2

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916 GGCACAGTGCAGCGCGGTGACCCAGGAGCGGCGCGCGCGCGCGCGCGCGAGAG 975  
301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320  
976 GAGCAGCCACTG-----CTGCCCTCCAGCGGCTTCAGCGGCTCGCAGCGCGCTCG 1023  
321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
1024 AGGCCCCGATCCCTTCCGCCCCCGAGAGGCTCAGCGGCTTCAGCGGCTCGCAGCG 1083  
341 AlaLeuAspTyrProSerGluAenLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
1084 GCGCTGGATTATCCCGAGAGAACCTGGCTTCATCGACGAGTCTCGGATACCGAGC 1143  
361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAenProSerLys 380  
1144 GAGCGGCGTGCCTGCGCGCGCGCGCGCGAGAGTCCCGCGCCCAATCCCGCCAGG 1203  
381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
1204 AGCCCGTGGCGTG 1257

RESULT 6  
US-09-828-035-1  
; Sequence 1, Application US/09828035  
; Patent No. US20020034781A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria A.  
; TITLE OF INVENTION: 12303, A NOVEL HUMAN TWIK MOLECULE AND USES THEREOF  
; FILE REFERENCE: WNI-142  
; CURRENT APPLICATION NUMBER: US/09/828, 035  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/195,734  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1408  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (84)...(1340)  
US-09-828-035-1

Alignment Scores: 4,02e-142 Length: 1408  
Pred. No.: 1692,50 Matches: 328  
Score: 88.44% Conservative: 24  
Percent Similarity: 82.41% Mismatches: 41  
Best Local Similarity: 81.41% Indels: 5  
Query Match: 9 Gaps: 2  
DB:  
US-09-655-272-2 (1-398) x US-09-828-035-1 (1-1408)  
Qy 1 MetArgSerThrThrLeuLeuAlaLeuAlaLeuValLeuLeuTyrLeuValSerGly 20  
Db 162 ATGCGCAGCACCACGCTCTGGCCCTGCTGGGCTGGTCTTCTTACTTGTGTGTGTGTGT 221  
Qy 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
Db 222 GCCCTGTGTTCGGGCGCTTGGAGCAGCCACACGAGCAGCAGCCAGGAGGAGCTGGGG 281  
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
Db 282 GAGGTCCGAGAGAAGTTCTCTGAGGCGCCATCCCTGTGTGTGAGCCAGCAGGAGCTGGCC 341  
Qy 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80  
Db 342 CTCATCAAGGAGGTGGCTGTATGCTTGGAGGGGTGGGACCCAGAACCAACCTCGACC 401  
Qy 81 AenSerSerAenHisSerSerAlaTrpAsnLeuGlySerAlaPheSerAlaPhePheSerGlyThr 100  
Db 402 AGCAACAGCAGCCAC---TCAGCCTGGGACCTGGGACGCGCTTCTTTTCTCAGGAGAC 458  
Qy 101 IleIleThrThrIleGlyTyrGlyValAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
Db 459 ATCATCACCACTATGGCTATGGCAATGTGGCCCTGGCAGATGCGGCGCGCTCTTC 518  
Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
Db 519 TGCACTTTTATGCTGTGGGATTCGCTGTGTGGATCTCTTCTGCTGATCGGC 578  
Qy 141 AspArgLeuGlySerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
Db 579 GACCGGCTGGGCTCTCTCTCGCATGGCATCGTTCATATTGAAGCATCTTCTTGAAG 638  
Qy 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180  
Db 639 TGGACGTGCCACCGGAGCTAGTAAGATGCTGTGCGGATGCTTCTCTGATCGGC 698  
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTyrSerLys 200  
Db 699 TGCCTGCTCTTGTCTCAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 758  
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220  
Db 759 CTGGAGGCCATCTACTTTGTCTAGTAGCTTACCACCGTTCGCGGCTTGGGCTGATGTG 818  
Qy 221 ProGlyAspGlyThrGlyGlnAenSerProAlaTyrGlnProLeuValTrpPheTrpIle 240  
Db 819 GCGGCGCGGACCCAGCAGGAGCTCCCGGCTATCAGCCGCTGGTGTGTGTGTGTGTGTG 878  
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAenTrpLeuArgAla 260  
Db 879 CTGCTCGGCGCTTACTTCTGCTCAGTGTCTCACCACCATCGGGAACCTGGCTGCGAGTA 938  
Qy 261 ValSerArgArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
Db 939 GTGTCCCGCGCATCTCGGCGAGATGGGCGGCTCAGCGCTCAGGCTCCAGCTGGACT 998  
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
Db 999 GGCACAGTGCAGCGCGTGCACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAG 1058  
Qy 301 GluGlnProLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320  
Db 1059 GAGCAGCCACTG-----CTGCCCTCCAGCGGCTTCAGCGGCGCGCGCGCTGGGC 1106



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Db 939 GTGTCCCGCCGCACTCGGCGAGAGATGGCGGCGCTCACGGCTCAGGCTGCCAGCTGGACT 998
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 999 GGCACAGTGCACGGCGGTGACCCAGCAGCGCGGCGCGCGCGCGCGGAGAG 1058
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 1059 GAGCAGCCACTG-----CTGCTCCACCGCCCTGTCCAGCGCGAGCGCGTGGGC 1106
Qy 321 ArgProGlySerProAlaProAlaGluValGluThrProSerProProThrAlaSer 340
Db 1107 AGGCCCGCATCCCTTCGCGCCCGAGAGAGCTACCGCGCTTCCCGCGCCAGCGCTCG 1166
Qy 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 1167 GCCCTGGATTATCCACGAGAGACCTGGCTTCATCGAGTCTCTCGGATACGAGAGC 1226
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
Db 1227 GAGCGCGCTGCCCGCTGCCCGCGCGCGCGAGAGGTGCCCGCGCCCAATCCCCCAGG 1286
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1287 AAGCCCGTGGCGCGCGCGCGCGCGCGCTCCCGAGACAAAGCGCTGCCGGTG 1340

RESULT 8
US-10-352-684A-7
; Sequence 7, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10317, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPT02-019P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: (84)....(1343)
US-10-352-684A-7
Alignment Scores: 4.02e-142 Length: 1408
Pred. No.: 1692.50 Matches: 328
Score: 88.44% Conservative: 24
Percent Similarity: 82.41% Mismatches: 41
Best Local Similarity: 81.41% Indels: 5
Query Match: 15 Gaps: 2
DB:

US-09-655-272-2 (1-398) x US-10-352-684A-7 (1-1408)
Qy 1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuTyrLeuValSerGly 20
Db 162 ATGCGCAGCACCAGCTCTCGGCGCTGTCTGTCTTACTTGTGTGTCTGTGT 221
Qy 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnAlaGlnInLysLysMetAsp 40
Db 222 GCCCTGGTGTTCGGGCGCTGGAGCAGCCACAGCAGCAGCGCCAGAGGGAGCTGGG 281
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 282 GAGTCCGAGAGAGTTCCTGAGGGCCATCCGCTGTGTGAGCGCAGCAGGAGCTGGG 341
Qy 61 PheLeuLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 342 CTCATCAGAGAGTGGCTGATGCTCGGCGGGGTGCGGACCGGCGCTTCTTTTCTCAGG 401
Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 402 AGCAACAGCAGCCAC---TCAGCTCGGAGCCTGGCGCGCGCTTCTTTTCTCAGGAG 458
Qy 101 IleIleThrThrIleGlyTyrGlyAsnLeuValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 459 ATCATCACACCATCGCTATGCAATGTGGCAATGTGGCCCTGCGCAGATGCGCGCGCTCT 518
Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 519 TGCATCTTTTATGCGCTCGTGGGATTCCTCGTGTGGATCTTACTTGGCAGGGGTGGG 578
Qy 141 AspArgLeuGlySerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 579 GACCGGCTGGGCTCTCTCCCTGCGCATCGCTACATTTGAAGCCATCTTCTTGAAG 638
Qy 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 639 TGGCAGTCCACCGGAGCTAGTAAGAGTGTGTGCGGATGCTTTTCTGCTGATCGGC 698
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 699 TGCCTGCTCTTTTGTCTCTACGCGCCAGCTTACCGCGCTATCAGCCGCTGTGTGTGT 758
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
Db 759 CTGGAGGCCATCTACTTGTGTATGACGCTTACCGCGTGGGCTTTGGCGACTATGTG 818
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 819 GCCGGCGCGGAGCCCGCAGGAGGACTCCCGCGCTATCAGCCGCTGTGTGTGTCTGATC 878
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 879 CTGCTCGGCTGGCTTACTTCGCTCAGTGTCTCAGCCATCCAGGAGCTGGGCTGGAGTA 938
Qy 261 ValSerThrArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 939 GTGTCCCGCGCACTCGGCGAGAGATGGCGGCGCTCACGGCTCAGGCTGCCAGCTGACT 998
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 999 GGCACAGTGCACGGCGCGTGCACCGAGAGCGCGCGCGCGCGCGCGGAGAG 1058

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Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 1059 GAGAGCCACTG-----CTGCCTCCACCGCCCTGTCCAGCGCAGCGCTGGC 1106
Qy 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340
Db 1107 AGGCCCGCATCCCTTCGCCCGGAGAGGCTCAGCGGCTTCCCGCCACAGCGCTCG 1166
Qy 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 1167 GCCTCGATTATCCAGCAGAACCTGCCTTCATCAGCAGTCTCTCGATACGAGC 1226
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
Db 1227 GAGCGCGCTGCCCGCTGCCCGCGCGCGAGAGGTGCGCGCGCCCAAAATCCCCAGG 1286
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1287 AGCCCCGTGCGGCCCCCGCGCGCGCGCTCCCGAGACAAAGCGTGCCGGTG 1340

RESULT 9
US-10-391-399-18
; Sequence 18, Application US/10391399
; Publication No. US20030219806A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Lora, Jose M.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: NOVEL 18607, 15603, 69318, 12303, 48000,
; TITLE OF INVENTION: 52920, 5433, 38554, 57301, 58324, 55063, 52991, 59914, 59921
; TITLE OF INVENTION: AND 33751 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0200NM
; CURRENT APPLICATION NUMBER: US/10/391,399
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/789,481
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 09/634,669
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 09/583,373
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/510,706
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 10/309,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/336,936
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 10/094,214
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US60/275,078
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)...(1343)
US-10-391-399-18

Alignment Scores:
Pred. No.: 4.02e-142 Length: 1408
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
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Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 15 Gaps: 2
US-09-655-272-2 (1-398) x US-10-391-399-18 (1-1408)
Qy 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20
Db 162 ATCGCAGCAGCAGCAGCTCTGGCCCTGTGGCGCTGTCTTGTCTTGTCTGTCTGT 221
Qy 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnAlaGlnLysLysMetAsp 40
Db 222 GCCTCGTGTTCGGGCGCTGGAGCAGCCCGCAGCAGCAGCAGCAGGAGCTGGGG 281
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 282 GAGGTCCGAGAGAGTTCCTGAGGGCCCATCCGTGTGTGAGCGACACGAGGCTGGGCTC 341
Qy 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerThr 80
Db 342 CTCATCAAGAGAGGTGCTGATGCCCTGGGAGGGGTGCGGACCCAGAAACCACTCGACC 401
Qy 81 AsnSerSerAsnHisSerSerAlaTyrAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 402 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGGCGCGCTCTCTTTTCTCAGGACC 458
Qy 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 459 ATCATCACCAACCATCGCTATGGCAATGTGGCCCTGGCCACAGATGCCGGCGCCTTTC 518
Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 519 TGCATCTTTATGCGCTGTGGGATTCGCTCTTTGGGATCTTACTGGCAGGGCTGGG 578
Qy 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 579 GACCGCTGGGCTCTCTCCCTGGCCCATGGCATCGTCACATTAAGCCATCTTCTTGAAG 638
Qy 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 639 TGGCAGCTGCCACCGGAGCTAGTAAGAGTGTGTGGCGATGCTTTTCTGTGATCGGC 698
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerThrSerLys 200
Db 699 TGCCTGCTCTTTGCTCTCACGCCCACTGCTGTCTGTATATGAGGACTGGAGCAAG 758
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
Db 759 CTGAGGCGCATCTACTTTGTATAGTACGCTTACCACCGTGGGCTTTGGCGACTATGTG 818
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 819 GCCGGCGCGGACCCCGAGGAGGACTCCCGGCTATCAGCGCTGTGTGTGTCTGGATC 878
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 879 CTGCTCGGCTGCGCTTACTTTCGCTCAGTGCTCACCACCATCGGAACCTGGCTCGCAGTA 938
Qy 261 ValSerArgArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaIleAlaSerTrpThr 280
Db 939 GTGTCCCGCGCAGCTCGGCGAGATGGGCGGCTCACGGCTCAGGCTGCCAGCTGCAGT 998
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 999 GGCACAGTGCAGCGCGCTGACCCAGCAGCGCGGCGCGCGCGCGCGCGCGGAGAG 1058
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 1059 GAGAGCCACTG-----CTGCCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 1106
Qy 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340
Db 1107 AGGCCCGCATCCCTTCGCCCGGAGAGGCTCAGCGGCTTCCCGCCACAGCGCTCG 1166
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341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
1167 GCCTGGATTATCCAGGAGAACCTGGCCCTTCATCGACGAGTCTCGGATACGCAGAGC 1226
361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380
1227 GAGCGCGCTGCCGCTGCCCGCGCGCGAGAGGTGCGCGCCGCAATCCCCAGG 1286
381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
1287 AGCCCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTG 1340

RESULT 10
US-10-768-158-11
; Sequence 11, Application US/10768158
; Publication No. US20040204359A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliassof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 16386, 15402, 21165, 1423,
; TITLE OF INVENTION: 636, 12303, 21425, 27410, 38554, 38555, 55063, 57145, 59914,
; TITLE OF INVENTION: 94921, 16852, 33260, 58573, 30911, 85913, 14303, 16816,
; TITLE OF INVENTION: 17827 OR 32620
; FILE REFERENCE: MP103-012P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10768,158
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,781
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/452,291
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/454,540
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 60/478,805
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/491,048
; PRIOR FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2747
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)...(1310)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2747)
; OTHER INFORMATION: n = A,T,C or G
US-10-768-158-11

Alignment Scores:
Pred. No.: 9,17e-142 Length: 2747
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 18 Gaps: 2

US-09-655-272-2 (1-398) x US-10-768-158-11 (1-2747)

Qy 1 MetArgSerThrThrLeuLeuAlaLeuAlaLeuValLeuLeuTyrLeuValSerGly 20
Db 129 ATCGCAGCAGCACCGCTCTGCGCCCTGCTGGCGCTGCTTCTTACTTGTGTGTGT 188
Qy 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAsp 40
Db 189 GCCTGTGTGTTCGGGCGCTTGGAGAGCCCGCAGCAGCAGCGCGCGAGGAGGTGGG 248

41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
249 GAGTCCGAGAGAGTTCTCTGAGGGCCCATCCGTGTGTGAGCGACACGAGGAGCTGGG 308
61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
309 CTCATCAAGAGGTGGGTGATGCTCGGAGGGGGTGGGACCCAGAAACAACCTCGACC 368
81 AsnSerSerHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
369 AGCAACAGACCCAC--TCAGCCTGGAGCTGGGACGCGCTCTCTTTTCTCAGGGACC 425
101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
426 ATCATCACCACTCGGCTATGTCATATGTGGCCCTGGCCACAGATGCGGGCGCTCTTC 485
121 CysIlePheTyrAlaLeuValGlyLysLeuPheGlyMetLeuLeuAlaGlyValGly 140
486 TGCATCTTTTATGCGCTGGTGGGATTCCTCGCTGTTTGGGATCTCTTCTGGCAGGG 545
141 AspArgLeuGlySerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
546 GACCGCTGGGCTCTCTCGCCATGCGCATCGGTACATTGAAGCCATCTTCTTGAAG 605
161 TrpHisValProGlyValLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
606 TGGCAGCTGCCACCGAGCTAGTAAGAGTGTGTGGGATGCTTTCTTCTGCTGATCGGC 665
181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
666 TGCCTGCTCTTTGCTCTCAGCCCACTGTTCTGTTCTCTATATGAGGAGCTGGAGCAAG 725
201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
726 CTGGAGGCCATCTACTTGTTCATAGTACGCTTACACCGCTGGGCTTTGGGAGCTATGTG 785
221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
786 GCCGCGCGGACCCCGAGGAGGACTCCCGCGGCTATCAGCGCTGTGTGTGTCTGGATC 845
241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
846 CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTCACCACTCGGAACTGGGTGGAGTA 905
261 ValSerArgArgThrArgAlaGluMetGlyLeuThrThrAlaGlnAlaAlaSerTrpThr 280
906 GTGTCCCGCGCAGCTCGGCGAGATGGGCGGCTCACGGCTCAGGCTGCCAGCTGGACT 965
281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
966 GGCACAGTGACAGCGCGCTGACCCAGCGAGCGGCGCGCGCGCGCGCGCGGAGAG 1025
301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValGluProAlaGly 320
1026 GAGCAGCCACTG-----CTGCCCTCACCGCCCTGTCCAGCGCGCGCTGGGC 1073
321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340
1074 AGGCCCCGATCCCTTCGCCCGCCCGAGAGGCTCAGCGGCTTCCCGCGCGCGGCTCG 1133
341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
1134 GCCTGGATTATCCAGGAGAACCTGGCCCTTCATCGACGAGTCTCTCGGATACGCAGAGC 1193
361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380
1194 GAGCGCGCTGCCGCTGCCCGCGCGCGAGAGGTGCGCGCGCGCGCGCGCGCGCGAGG 1253
381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
1254 AAGCCCGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTG 1307

RESULT 11
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US-10-345-680-43  
; Sequence 43, Application US/10345680  
; Publication No. US20030148394A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Venkateswarlu, Karicheti  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,  
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,  
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18936, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MP102-012P1RM OMNI  
; CURRENT APPLICATION NUMBER: US/10/345,680  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/423,809  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/429,797  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 2772  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (64)...(1323)  
US-10-345-680-43

Alignment Scores:  
Pred. No.: 9,28e-142 Length: 2772  
Score: 1692.50 Matches: 328  
Percent Similarity: 88.44% Conservative: 24  
Best Local Similarity: 82.41% Mismatches: 41  
Query Match: 81.41% Indels: 5  
DB: 15 Gaps: 2

US-09-655-272-2 (1-398) x US-10-345-680-43 (1-2772)

Qy 1 MetArgSerThrLeuLeuAlaLeuLeuValLeuLeuTyrLeuValSerGly 20  
Db 142 ATGGCAGACCAAGTCTCTGGCCCTCTGCGCTGCTTCTTTCTTTCTGGT 201  
Qy 21 AlaLeuValPheGlnAlaLeuGlnProHisGlnGlnAlaGlnLysLysMetAsp 40  
Db 202 GCCCTGGTGTTCGGGCGCTTGGAGCACCCACAGCAGGAGGAGGAGGAGGAGG 261  
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuLeuAsp 60  
Db 262 GAGTCCGAGAGAAGTCTCTGAGGCCCATCCGTGTGTGAGCACGAGGAGCTGGGCTC 321  
Qy 61 PheIleLysLeuLeuValGlnAlaLeuGlyGlyGlyAlaLeuAlaLeuThrSerTrpThr 80  
Db 322 CTATCAAGAGGTGGTGTGATGCCCTGGAGGGGGTGGGAGCCAGAAACCAATCGACC 381  
Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
Db 382 AGCAACAGCAGCCAC-----TCAGCCTGGGACCTGGGAGCGCCTCTTTTCTAGGGACC 438

Qy 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuLeuHisThrAspAlaGlyArgLeuPhe 120  
Db 439 ATCATCACCACTCGCTATGGCAATGTGGCCCTGCGCACAGATCGCGGCGCTCTTC 498  
Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
Db 499 TGCAATCTTCTATGCGCTGGTGGGANTCCGCTGTTGGGATCTCTACTGGCAGGGGTGGG 558  
Qy 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
Db 559 GACCGGCTGGGCTCTCTCCCTGCGCCATGGCATCGGTACATTGAAGCCATCTTCTTGAAG 618  
Qy 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuLeuLeuLeuGly 180  
Db 619 TGGACGCTGCCACCGAGCTAGTAGAGTGTCTGCGGATGCTTTCTTCGTGATCGGC 678  
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
Db 679 TGCCTGCTCTTGTCTCTACGCCCATGTTGCTGTTCTGTATATGAGGACTGGAGCAAG 738  
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTrpVal 220  
Db 739 CTGGAGGCCATCTACTTTGTATAGTACGCTTACCACCGTGGCTTTGGCGCATATGTG 798  
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240  
Db 799 GCCGGGCGGACCCCGAGGAGGATCCCGGCTATCAGCCGCTGTTGTGTTCTGGATC 858  
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
Db 859 CTGCTCGGCTGGCTTACTTTCGCTCAGTGCTCACCACCATCGGAACTGGCTGGAGTA 918  
Qy 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
Db 919 GTGTCGCGCGCACTCGGGCAGAGATGGGCGGCTCAGCGCTCAGGCTGCAGCTGGACT 978  
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
Db 979 GGCACAGTGACAGCGGCGGTGACCCAGCAGCGGCGGCGCGCGCGCGCGCGGAGG 1038  
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320  
Db 1039 GAGCAGCCACTG-----CTGCCCTCCACCGCCCTGTCCAGGCGAGCGCTGGGC 1086  
Qy 321 ArgProGlySerProAlaProAlaGluLysValGlyValThrProSerProThrAlaSer 340  
Db 1087 AGSCCGGATCCCTTTCGCCCCCGAGAGGCTCAGCTGCTTCCCGCGCCACCGGCTCG 1146  
Qy 341 AlaLeuAspTyrProSerGluLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
Db 1147 GCCCTGGATTATCCAGCGAGAACCTGGCCTTCATCAGCAGGTCTCTGGATACGACAGC 1206  
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380  
Db 1207 GAGCGGCGCTGCCCGCTGCGCGCGCGGAGAGGTGCGCGCGCCCAATCCCGGAGG 1266  
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
Db 1267 AAGCCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1320

## RESULT 12

US-09-747-835A-30  
; Sequence 30, Application US/09747835A  
; Patent No. US20020146692A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyun  
; APPLICANT: Asundi, Vinod

Alignment Scores:	3,27e-141	Length:	3945
Pred. No.:	1698.50	Matches:	327
Score:	88.41%	Conservative:	24
Percent Smilarity:	82.37%	Mismatches:	41
Best Local Similarity:	81.22%	Indels:	5
Query Match:	9	Gaps:	2
DB:			
US-09-655-272-2 (1-398) x US-09-747-835A-30 (1-3945)			
Qy	1	MetArgSerThrLeuLeuAlaLeuValLeuValLeuYrLeuValSerGly	20
Db	1618	ATGGCGAGCACCAGCTCTGGCCCTGCTGGCGCTGGTCTGTCTTACTTGGTGTCTGGT	1677
Qy	21	AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnIysLysMetAsp	40
Db	1678	GCCCTGGTGTTCGGGGCCCTGGACGCCCCACAGCAGAGGCCACAGAGGAGCTGGGG	1737
Qy	41	HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnIysSerLeuGluAsp	60
Db	1738	GAGTCCGAGAGAGATTCTTGAGGGCCCATCCGTTGTGTGAGCGCACGAGAGCTGGGCCCTC	1797
Qy	61	PheIleLysLeuValGluAlaLeuGlyGlyGlyAlaasnProGluThrSerTrpThr	80
Db	1798	CTCATCAAGGAGTGCGCTGATGCCCTGGAGGGGGTGGGACCCAGAAACCACTCGACC	1857
Qy	81	AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr	100
Db	1858	AGCAACAGCAGCCAC--TCAGCTGGGACCTGGGCGCGCTCTTTTCTCAGGGACC	1914
Qy	101	IleIleThrThrIleGlyTyrcGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe	120
Db	1915	ATCATCACCATCGGCTATGGCAATGTGGCCCTGGCCACAGATGCCGGCGGCTCTTC	1974
Qy	121	CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly	140
Db	1975	TGCATCTTTATGCGCTGGTGGGATTCGCTGTTTGGATCCTACTGCCAGGGGTCCGG	2034
Qy	141	AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys	160
Db	2035	GACCGGCTGGGCTCTCCCTGGGCCATGGCATCGGTGCATTTGAAGCCATCTTCTTGAG	2094
Qy	161	TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly	180
Db	2095	TGGCAGCTGCCACGGGAGCTAGTAAGAGTGTGTGGCGCATCTTCTCTGCTGATCGGC	2154
Qy	101	MetArgSerThrLeuLeuValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys	200

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; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 30
; LENGTH: 3945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-312-312-30

Alignment Scores:
Pred. No.: 3,27e-141 Length: 3945
Score: 1688.50 Matches: 327
Percent Similarity: 88.41% Conservative: 24
Best Local Similarity: 82.37% Mismatches: 41
Query Match: 81.22% Indels: 5
DB: 16 Gaps: 2

US-09-655-272-2 (1-398) x US-10-312-312-30 (1-3945)

Qy 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuValLeuLeuValSerGly 20
Db 1618 ATGGCAGACACCGCTCTGGCCCTGCTGGCGCTGCTTGTCTTACTTGGTCTGCT 1677
Qy 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40
Db 1678 GCCCTGGTGTTCGGGGCCCTGGAGCAGCCCGCAGCAGCAGCCCGCAGAGGGAGCTGGGG 1737
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 1738 GAGGTCCGAGAGAGTTCCTGAGGGCCCATCGGTGTGTGAGCAGCAGGAGCTGGGCCTC 1797
Qy 61 PheileLysLeuLeuValGlnAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 1798 CTCATCAAGAGGTGGCTGATCCCTGGAGGGGTGCGGACCAGAAACCACTCGACC 1857
Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 1858 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGCAGCGCCCTCTTTTCTCAGGACC 1914
Qy 101 IleileThrThrileGlyTyrglyValenileValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 1915 ATCATCACCACTCGGTATGCAATGGCCCTGGCAGACATGCGGGCCCTCTTC 1974
Qy 121 CysilePheTyralaLeuValGlyileProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 1975 TGCATCTTTTATGCGCTGGTGGGATTCCTGCTGTTGGGATCCTACTGGCAGGGTCGG 2034
Qy 141 AspArgLeuGlySerSerLeuArgArgGlyileGlyHisileGluAlallePheLeuLys 160
Db 2035 GACCGGCTGGGCTCCTCCCTGCGCCATGGCATCGGTACATTTGAAGCCATCTTTTGAAG 2094
Qy 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuileGly 180
Db 2095 TGCACGTGTCACCGAGCTAGTAAGAGTCTGTGCGGATGCTTTTCTGCTGATCGGC 2154
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrrMetGluSerTrpSerLys 200
Db 2155 TGCCTGCTCTTGTCTCCTCGCCACCGCTTGTCTGTCTATGAGGAGCTGAGCAAG 2214
Qy 201 LeuGluAlalleTyrrPheValilleValThrLeuThrThrValGlyPheGlyAspTyrrVal 220
Db 2215 CTGGAGCCCATCTACTTGTATAGTACGCTTACCACCGTGGCTTTGGCGACTATGTG 2274
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrrGlnProLeuValTrpPheTrpIle 240
Db 2275 GCCGGCGGAGCCCGAGGAGACTCCCGGCGCTATCAGCGCTGTGGTGTCTGATC 2334
Qy 241 LeuPheGlyLeuAlaTyrrPheAlaSerValLeuThrThrileGlyAsnTrpLeuArgAla 260
Db 2335 CTGCTCGGCTGGCTTACTTCTGCTCAGTGTCTCAGCAGCAGCAGTGGCTGGCAGTA 2394
Qy 261 ValSerArgArgThrArgAlaGluMetGlyLeuThrThrAlaGlnAlaSerTrpThr 280

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Db 2395 GTGTCCCGCGCAGCTCGGCGAGATGGGGCGCTTACGGCTCAGGCTGCAGCTGACT 2454
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProProGluLys 300
Db 2455 GGCACAGTGACAGCGCGGTGACCCAGGAGCGCGGCCCGCCCGCCCGCGGAGAAG 2514
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 2515 GAGCAGCCACTG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 2562
Qy 321 ArgProGlySerProAlaProAlaGluLeuValGluThrProSerProProThrAlaSer 340
Db 2563 AGGCCCGGATCCCTTTCGCCCCCGGAGAGGCTCAGCGGCTTCCCGCCCGCAGCGCTCG 2622
Qy 341 AlaLeuAspTyrrProSerGluAsnLeuAlaPheileAspGluSerSerAspThrGlnSer 360
Db 2623 GCCCTGATATCCAGCGAGAACCTGCGCTTCATCGAGAGTCTCGGATACGCAGAGC 2682
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
Db 2683 GAGCGGGGCTGCGCTGCGCGCGCGGAGAGGTGCGCGCGCCCAATCCCGCCAGG 2742
Qy 381 LysProSerArgProArgGlyProGlyArgGlyLeuArgAspLysAlaValPro 397
Db 2743 AGCCCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2793

RESULT 14
US-09-747-835A-28
; Sequence 28, Application US/09747835A
; Patent No. US20020146692A1
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Asundi, Vinod
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
; TITLE OF INVENTION: (LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-37CIP
; CURRENT APPLICATION NUMBER: US/09/747,835A
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/729,739
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 28
; LENGTH: 3996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3996)
US-09-747-835A-28

Alignment Scores:
Pred. No.: 3,32e-141 Length: 3996
Score: 1688.50 Matches: 327
Percent Similarity: 88.41% Conservative: 24

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Thu Feb 3 07:31:02 2005

Best Local Similarity: 82.37% Mismatches: 41  
 Query Match: 81.22% Indels: 5  
 DB: 9 Gaps: 2

US-09-655-272-2 (1-398) x US-09-747-835A-28 (1-3996)

QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuValLeuLeuValSerGly 20  
 Db 1669 ATGCGGACACACAGCTCTGCGCCCTGCTGGCGCTGCTCTTCTTACTTGTGTCTGT 1728

QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysMetAsp 40  
 Db 1729 GCCTGTGTTCGGGCGCTGGAGAGCCCGACGAGCAGCCCGAGGAGCTGGGG 1788

QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 Db 1789 GAGTTCGAGAGAGAGTTCCTGAGGGCCCATCGGTGTGTGAGGAGCCAGGAGCTGGGCTC 1848

QY 61 PheLeuLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
 Db 1849 CTCATCAAGGAGGTGGTGTATGCTTGGAGGGGTGGGACCCAGAAACCAACTCGACC 1908

QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 Db 1909 AGCAACAGCAGCCAC---TCAGCCTGGGACCTGGGAGCGCTCTTTTTCACAGGACC 1965

QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 Db 1966 ATCATCACCACCATCGCTATGCAATGTGGCCCTGGCACAGATGCCGGGCGCTCTTC 2025

QY 121 CysIlePheTyrAlaLeuValGlyLeuProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
 Db 2026 TGCATCTTTTATGCGTGTGGGATTCGCTGTGTGGGATCTCTGAGGAGGCTCGG 2085

QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 Db 2086 GACCGGCTGGGCTCTCTCTGGCATGCGATCGCTCACATTTGAAGCATCTCTTTGAAG 2145

QY 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180  
 Db 2146 TGGCAGCTGCCACCGAGCTAGTAGAGTGTGTGGGATGTCTTTCTGCTGATCGGC 2205

QY 181 CysLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
 Db 2206 TGCTGTCTTTTGTCTCTACGCCACGTCGTGTCTATATGAGGAGCTGGAGCAAG 2265

QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220  
 Db 2266 CTGGAGGCACTACTTTGTCTATAGTACGCTTACACCGTGGGCTTTGGCGACTATGTG 2325

QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240  
 Db 2326 GCGGCGCGGACCCAGGAGGACTTCCCGGCTATACGCGCTGTGTGTGTCTGGATC 2385

QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
 Db 2386 CTGCTGGCTGGCTTACTTGGCTCAGTGTCTCACCCATCGGAATGCTGGAGTA 2445

QY 261 ValSerArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 Db 2446 GTGTCCCGCGCACTCGGGCAGAGATGGGCGGCTTACGGCTCAGGCTGCCAGCTGGACT 2505

QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 Db 2506 GGCACAGTGACGGCGGTGACCCAGGAGCGCGGCGCGCGCGCGCGCGGAGAG 2565

QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320  
 Db 2566 GAGCAGCACTG-----CTGCCCTCCACCGCCCTGTCCACCGAGCGGCTGGGC 2613

QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340  
 Db 2614 AGGCCCGCATCCCTTCGCGCCCGCCGAGAGGCTCAGCGCGCTTCCCGCGCCCGGCTCG 2673

RESULT 15

US-10-037-270-195  
 ; Sequence 195, Application US/10037270  
 ; Publication No. US20030104529A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Liu, Chenghua  
 ; APPLICANT: Asundi, Vinod  
 ; APPLICANT: Zhang, Jie  
 ; APPLICANT: Ren, Feiyan  
 ; APPLICANT: Chen, Rui-hong  
 ; APPLICANT: Zhao, Qing A.  
 ; APPLICANT: Wehrman, Tom  
 ; APPLICANT: Xue, Aidong J.  
 ; APPLICANT: Yang, Yonghong  
 ; APPLICANT: Wang, Jian-Rui  
 ; APPLICANT: Zhou, Ping  
 ; APPLICANT: Ma, Yundong  
 ; APPLICANT: Wang, Dunrui  
 ; APPLICANT: Wang, Zhiwei  
 ; APPLICANT: Tillinghaast, John  
 ; APPLICANT: Drmanac, Radoje T.  
 ; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and  
 ; TITLE OF INVENTION: Polypeptides  
 ; FILE REFERENCE: 78AC1P2B  
 ; CURRENT APPLICATION NUMBER: US/10/037,270  
 ; CURRENT FILING DATE: 2002-01-04  
 ; PRIOR APPLICATION NUMBER: 09/552,317  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: 09/488,725  
 ; PRIOR FILING DATE: 2000-01-21  
 ; NUMBER OF SEQ ID NOS: 1104  
 ; SOFTWARE: pt\_FL\_genes Version 1.0  
 ; SEQ ID NO 195  
 ; LENGTH: 3996  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (52)..(3996)  
 ; US-10-037-270-195

Alignment Scores:  
 Pred. No.: 3,32e-141 Length: 3996  
 Score: 1688.50 Matches: 327  
 Percent Similarity: 88.41% Conservative: 24  
 Best Local Similarity: 82.37% Mismatches: 41  
 Query Match: 81.22% Indels: 5  
 DB: 15 Gaps: 2

US-09-655-272-2 (1-398) x US-10-037-270-195 (1-3996)

QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuValLeuLeuValSerGly 20  
 Db 1669 ATGCGGACACACAGCTCTGCGCCCTGCTGGCGCTGCTCTTCTTACTTGTGTCTGT 1728

QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysMetAsp 40  
 Db 1729 GCCTGTGTTCGGGCGCTGGAGAGCCCGACGAGCAGCCCGAGGAGCTGGGG 1788

Search completed: February 3, 2005, 06:54:04  
Job time : 711.536 secs

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QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnIlySerLeuGluAsp 60
Db 1789 GAGGTCGAGAGAAAGTTCCTGAGGGGCCCATCCGTGTGTGAGCGACACGAGGCTGGGCCTC 1848
QY 61 PheIleLeuLeuValGluAlaLeuGlyGlyGlyValaAsnProGluThrSerTrpThr 80
Db 1849 CTCAATCAGGAGGTGGCTGATGCCCTGGAGGGGGTGGGAGCCAGAAACCAACTCGACC 1908
QY 81 AsnSerSerAsnHisSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 1909 AGCAACAGCAGCCAC--TCAGCCTGGACCTGGCAGCGCCTCTCTTTCTCAGGGACC 1965
QY 101 IleIleThrThrIleGlyThrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 1966 ATCATCACCACCATCGGCTATGGCAATGTGGCCCTGCGCACAGATGCCGGGGCCCTCTTC 2025
QY 121 CysIlePheTrpAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 2026 TGCATCTTTTATCGCTGGTGGGGATTCGCTGTTTGGGATCCTACTGGCAGGGGTTCGGG 2085
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 2086 GACCGGCTGGGCTCCTCCCTCGGCCATGGCATCGGTACATTGAAGCCATCTTCTTTGAAG 2145
QY 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 2146 TGGCAGCTGTCACCGGAGCTAGTAAGAGTGTCTGCGCGATGCTTTTCTGTGATCGGC 2205
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTrpMetGluSerTrpSerLys 200
Db 2206 TGCCTGCTCTTTGCTCTCAGCCCAAGTTCGTGTTCTGTATATGAGGACTGGAGCAAG 2265
QY 201 LeuGluAlaIleTrpPheValIleValThrLeuThrThrValGlyPheGlyAspTrpVal 220
Db 2266 CTGGAGGCCATCTACTTGTATAGTACGCTTACCACCGTGGGCTTTGGCGACTATGTG 2325
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTrpGlnProLeuValTrpPheTrpIle 240
Db 2326 GCGGGCGCGGACCCAGCAGGAGTCCCGCGCTATCAGCGCTGGTGTGTGTTCTGGATC 2385
QY 241 LeuPheGlyLeuAlaTrpPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
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QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 2446 GTCTCCGCGGCACTCGGGCAGAGATGGCGGCTCAGCGCTCAGGCTGCCAGCTGGACT 2505
QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 2506 GGCACAGTGACAGCGGCGTGTAGCCAGCGAGCGGGCCCGCGCCCGCGCGGAGAG 2565
QY 301 GluGlnProLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320
Db 2566 GAGCAGCCACTG-----CTGCCCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 2613
QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340
Db 2614 AGGCCCCGATCCCTTCGCCCCCGGAGAGGCTCAGCGGCTTCCCGCCACGCGCTCG 2673
QY 341 AlaLeuAspTrpProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 2674 GCCCTGGATTATCCACGAGAACCTGGCCTTCATCGACGAGTCTCGGATACGACAGC 2733
QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
Db 2734 GAGCGGCGCTGCCCGCTGCCCGCGCGCCGAGAGGTCCCGCGCCCAATAATCCCCCAGG 2793
QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValPro 397
Db 2794 AAGCCCGTGGCGGCCCGCGGCCCGCGGCGTCCCCGAGACAAAGCGGTGCGG 2844
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 21:56:31 ; Search time 4055.14 Seconds

(without alignments)  
3576.449 Million cell updates/sec

Title: US-09-655-272-2

Perfect score: 2079

Sequence: 1 MKSTTLALLLVLLVLSG.....SKKPSRPRGRLDKAVPV 398

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gseq.\*  
9: gb\_gseq2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2079	100.0	1197	9	AY405806 Mus muscu
2	1692.5	81.4	1182	9	AY405804 Homo sapi
3	1381	66.4	1560	3	CR603880 full-leng
4	1187	57.1	1405	3	BC067791 Homo sapi
5	986	47.4	581	6	CB606856 AMGNNUC:N
6	907	43.6	590	2	BE981482
7	898	43.2	736	5	EX451513
8	822.5	39.6	922	4	BI758226

10	802	38.6	2534	3	AK082153	AK082153 Mus muscu
11	788	37.9	1745	3	AK036066	AK036066 Mus muscu
12	785	37.8	2628	3	AK031904	AK031904 Mus muscu
13	784	37.7	1113	9	AY418067	AY418067 Mus muscu
14	778	37.4	1113	9	AY418065	AY418065 Homo sapi
15	760	36.6	469	2	BF565047	BF565047 UI-R-B01-
16	717.5	34.5	891	1	AL537214	AL537214 AL537214
17	684	31.9	570	2	BB569111	BB569111 BB569111
18	656.5	31.6	922	7	CK653558	CK653558 AGENCOURT
19	618.5	29.7	1113	9	AY418066	AY418066 Pan trogl
20	618	29.7	802	1	AL537215	AL537215 AL537215
21	557.5	26.8	654	7	CK005597	CK005597 AGENCOURT
22	536	25.8	920	5	BQ948206	BQ948206 AGENCOURT
23	523.5	25.2	667	5	BU759620	BU759620 UI-R-PF0-
24	510.5	24.6	537	5	EX478651	EX478651 DKFP686H
25	494	23.8	627	7	CO039400	CO039400 UI-M-BH0-
26	491.5	23.6	879	9	AY404471	AY404471 Mus muscu
27	491	23.6	772	6	CB959623	CB959623 AGENCOURT
28	490	23.6	885	9	AY404469	AY404469 Homo sapi
29	486	23.4	553	5	BM942654	BM942654 UI-M-CG0P
30	484	23.3	498	6	BY248534	BY248534 BY248534
31	481.5	23.2	406	6	CB808226	CB808226 AMGNNUC:S
32	461.5	22.2	713	6	CB526721	CB526721 UI-M-PY0-
33	456.5	22.0	609	1	AU177116	AU177116 AU177116
34	447.5	21.5	479	6	CA871490	CA871490 K0910F08-
35	442.5	21.3	805	7	CK870719	CK870719 AGENCOURT
36	432.5	20.8	845	6	CD326083	CD326083 AGENCOURT
37	428.5	20.6	1491	3	CR622971	CR622971 full-leng
38	428.5	20.6	1493	3	CR626629	CR626629 full-leng
39	423.5	20.4	1129	4	BM544559	BM544559 AGENCOURT
40	421	20.3	3365	3	AK085330	AK085330 Mus muscu
41	416.5	20.0	775	7	CN528767	CN528767 UI-M-HQ0-
42	415.5	20.0	1360	3	AK019376	AK019376 Mus muscu
43	413.5	19.9	613	9	AY405805	AY405805 Pan trogl
44	413	19.9	801	5	BU304218	BU304218 603608750
45	412.5	19.8	4016	3	AK036882	AK036882 Mus muscu

#### ALIGNMENTS

RESULT 1	AY405806	1197 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	Mus musculus K0N4 gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	genomic survey sequence.				
ACCESSION	AY405806				
VERSION	AY405806.1	GI:39761780			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 1197)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBLISHED	14671302				
REFERENCE	2 (bases 1 to 1197)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment				
FEATURES	Location/Qualifiers				
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ORIGIN

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Score: 2079.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Gaps: 0

US-09-655-272-2 (1-398) x AY405806 (1-1197)

Qy 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuLeuValLeuValSerGly 20
Db 1 ATGGCGAGCAGCACACCTCTGGCTCTGCTGGCACTGGTGTCTTACCTTGGTATCTGGG 60

Qy 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAsp 40
Db 61 GCTCTAGTGTTCAGGCTCTGGAGCAGCTTCAGAGCAGGAGCTCAGAGAAATGGAT 120

Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 121 CATGGCGAGCAGCAGTTCCTGAGGAGCATCCCTGTGTGAGCAGAGAGCCTGGAGGAT 180

Qy 61 PheLeuLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 181 TTCATCAAGCTCTCTGGTGAAGCCCTGGAGGGGGCCAAACCCAGAAACACACCTGGACC 240

Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 241 AATAGCAGCAGCAGCAGTTCATCAGCTTGGAACTGGAGCCCTGCTCTTTCTCGGGGACC 300

Qy 101 IleLeuThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 301 ATCATCACTACCATCGGTATGGCAATATATGCTTACACAGATGCGGGCGTCTCTTT 360

Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 361 TGTATCTTCTATGCACTGGTGGGATCCACTGTTGGGATGCTGCTGGCGAGTGGG 420

Qy 141 AspArgLeuGlySerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 421 GACCGGTGGGCTCTCTCTGCGCGGGGCGCATCGGCCACATCGAAGCAATCTTCTTGAAG 480

Qy 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuIleGly 180
Db 481 TGGCATGTGCCACCGGGGTGGTGAGAGTCTGTCGGAGTGCTCTTCTCTGATCGGC 540

Qy 181 CysLeuLeuPheValLeuThrProPheValPheSerTyrMetGluSerTrpSerLys 200
Db 541 TGCTGCTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600

Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
Db 601 TTAGAAGCAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660

Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 661 CCCGGGATGGCAGCGGGCAGAGTCTCCAGGCTACAGCGCTGCTGTGTGTCTGTGATC 720

Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 721 TTGTTTGGCCTAGCTACTTCTGCTCAGTGCTCACCACCATCGGCACTGGTGTGGAGCA 780

Qy 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 781 GTGTCCCGCCGAACTCGGCGAGAGATGGTGGCTTAACGGCAGAGGCTCTAGCTGGACC 840

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281 GlyThrValThrAlaValThrGlnArgThrGlyProSerAlaProProGluLys 300
841 GGCACAGTACAGCGGAGTGACCCAGCGAATCGGCGCCAGCGCCGCGCAGAGAAG 900

301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValGluProAlaGly 320
901 GAGCAACCACTCTGCGCTCTCTTTGCGGCGCAGCCGCTGCTGTGTGAGCAGCGCGC 960

321 ArgProGlySerProAlaProAlaGluValGluThrProSerProProThrAlaSer 340
961 AGGCCCGGCTCTGCTGCGCGCAGAGAGTTTGACACTTCGCTCCCGCCGCGGCTCTCA 1020

341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
1021 GCTCTGGATTACCCAGTGAATCTGGCTTTCATGACGAGTCTCTCAGACACGAGAGT 1080

361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
1081 GAGCGTGGCTGTGCTGCTGCGGCTCTCGGGGTGCGCGGACCCCAACCATCCAA 1140

381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
1141 AAGCTTCCAGACCCCGGGTCTCTGGGCGACTCCGAGACAAGCGCTGCGCGGTG 1194

RESULT 2
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Homo sapiens KCNK4 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY405804 GI:39761778
VERSION AY405804.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1182)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1182)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity: 82.41%
Query Match: 81.41%
Indels: 5
Gaps: 2

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ORIGIN
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Pred. No.: 8,2e-80 Length: 1405
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Best Local Similarity: 70.66% Mismatches: 28
Query Match: 57.09% Indels: 55
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/note="Vector: pBluescript"

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DB 246 GTGCTGATCCCTGGGAGGGGTGGCGACCGAAGAACCACTCGACCAAGACAGCAGC 305
QY 85 HisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIleThrThr 104
DB 306 CAC---TCAGCCCTGGGACCTGGGAGCGCTCTTTTCTTCAGGGACCATCATCACACC 362
QY 105 IleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyr 124
DB 363 ATCGGTATGGCAATGGCCCTGGCACAGATCGCGGGCGCTCTTCGATCTTTAT 422
QY 125 AlaLeuValGlyIleProLeuPheGlyMetLeuAlaGlyValGlyAspArgLeuGly 144
DB 423 GCCTGTGGGGATTCCTGTTTGGGATCTACTGGCAGGGTCTGGGACCGGCTGGC 482
QY 145 SerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLysTrpHisValPro 164
DB 483 TCCTCCTGGCCATGCATCGCTCATATTGAAGCCATCTCTT----- 526
QY 165 ProGlyLeuValArgSerLeuSerAlaValLeuPheLeuIleGlyCysLeuLeuPhe 184
DB 526 ----- 526
QY 185 ValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLysLeuGluAlaIle 204
DB 526 ----- 526
QY 205 TyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrValProGlyAspGly 224
DB 527 -----GTGACGCTTACACCGTGGCTTGGCGACTATGTGGCGCGCGGAC 574
QY 225 ThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIleLeuPheGlyLeu 244
DB 575 CCAGGAGGACTCCCGGCTATCAGCGCTGGTGTCTTGGATCTGCTCGGCTG 634
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QY 265 ThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTrpThrGlyThrValThr 284
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QY 285 AlaArgValThrGlnArgThrGlyProSerAlaProProGluLysGluGlnProLeu 304
DB 755 GCGGGGTGACCCAGGAGCGGGCGCGCGCGCGCGCGCGAGAGAGAGAGAGAGAG 814
QY 305 LeuProSerSerLeuProAlaProAlaValValGluProAlaGlyArgProGlySer 324
DB 815 -----CTGCTCCACCGCCCTGTCCAGCGCAGCGCTGGGAGGCGCCCGATCC 862
QY 325 ProAlaProAlaGluLysValGluThrProSerProProThrAlaSerAlaLeuAspTyr 344
DB 863 CCTTCGCCCCCGAGAGGCTCAGCGCTTCCCGCCCAAGGCTCGGCTGGGATAT 922
QY 345 ProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSerGluArgGlyCys 364
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QY 385 ProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
DB 1043 CCGCGCGCGCGCGCGGTCCCGAGACAAAGGCGTCCCGGTG 1084
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LOCUS AMGNNUC.NRHY4-00145-Cl-A W Rat hypothalamus (10464) Rattus
DEFINITION norvegicus cDNA clone nrhy4-00145-cl 5', mRNA sequence.
ACCESSION CB060856
VERSION 1 GI:29546469
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 581)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00145 row: C column: 1.
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Score: 986.00 Matches: 186
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Best Local Similarity: 96.37% Mismatches: 5
Query Match: 47.43% Indels: 0
DB: 6 Gaps: 0
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DB 3 ATCAAGCTGTGCTGAAGCCCTGGGAGGGGCGCAACCCAGAACCAAGTTGACCAAT 62
QY 82 SerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIle 101
DB 63 AGCAGCAACCACTCATCAGCTTGGAACTGGGCGAGCGCTTCTTTCTCGGGGACCATC 122
QY 102 IleThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCys 121
DB 123 ATCACTTACATCGGCTACGCAATATAGCTTACACACAGATGCTGGGCGTCTCTTTGT 182
QY 122 IlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGlyAsp 141
DB 183 ATCTTCTATGACTGTGGGATGCCACATGTTCCGGATGCTGCTGGAGTCGGGAC 242
QY 142 ArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLysTrp 161
DB 243 CGGCTGGGCTCTCTCTGCGCGGGGATCGGTTCATCGACAGCATGTTCTTGAAGTGG 302
QY 162 HisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuIleGlyCys 181

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into the Not 1 and EcorV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
This sequence belongs to sequence cluster 6303.f  
For more information about this cluster, see  
[http://www.genoscope.cns.fr/cdna?8=CSOBAF015ZF10\\_AF01423\\_1&c=6303.f](http://www.genoscope.cns.fr/cdna?8=CSOBAF015ZF10_AF01423_1&c=6303.f)

# FEATURES

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## ORIGIN

Alignment Scores:  
Pred. No.: 3,14e-58 Length: 736  
Score: 898.00 Matches: 174  
Percent Similarity: 86.12% Conservative: 6  
Best Local Similarity: 83.25% Mismatches: 25  
Query Match: 43.19% Indels: 5  
DB: 5 Gaps: 1

US-09-655-272-2 (1-398) x BX451513 (1-736)

QY 190 pheValPheSerTyrMetGluSerTpsrLysLeuGluAlaIleTyrPheValIleVal 209  
DB 9 TTCGGTTCGTG-CTTATGAGGAGCTGAGCAAGCTGAGGCCATCTACTTTGTTCATAGTG 67  
QY 210 ThrLeuThrThrValGlyPheGlyAspTyrValProGlyAspGlyThrGlyGlnAenSer 229  
DB 68 ACGCTTACCACCGTGGCTTGGCGATGTGTGGCGCGCGAGCCAGGAGGACTCC 127  
QY 230 ProAlaTyrGlnProLeuValTpsrPheTrpIleLeuPheGlyLeuAlaTyrPheAlaSer 249  
DB 128 CCGGCGCTATCAGCGCTGTGTGTGTCTGGATCTCTCGGCTGTCTTACTTCGCTCA 187  
QY 250 ValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArgArgThrArgAlaGluMet 269  
DB 188 GTGCTCACCACCATCGGAACTGGCTGCGAGTAGTGTCCGCGCACTCGGCGAGAGTG 247  
QY 270 GlyGlyLeuThrAlaGlnAlaAlaSerTpsrThrGlyThrValThrAlaArgValThrGln 289  
DB 248 GCGGCGCTCAGGCTCAGGCTGCGAGTGGACAGTGCACAGTGCAGCGCGTGACCCAG 307  
QY 290 ArgThrGlyProSerAlaProProGluLysGluGlnProLeuLeuProSerSerLeu 309  
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QY 310 ProAlaProProAlaValValGluProAlaGlyArgProGlySerProAlaProAlaGlu 329  
DB 356 CTTCCACCGCGCTGTCCAGCGAGCGCTGGGCGAGCGCGCGAGTCCCTTCGCGCGCGAG 415  
QY 330 LysValGluThrProSerProProThrAlaSerAlaLeuAspTyrProSerGluAenLeu 349  
DB 416 AAGGCTCAGCGCGCTTCCCGCGCCAGCGGCTCGGCTGATTTATCCAGCGAGACCTG 475  
QY 350 AlaPheIleAspGluSerSerAspThrGlnSerGluArgGlyCysAlaLeuProArgAla 369  
DB 476 GCCTTCATCGACGAGTCTCGATACGACGAGCGAGCGGCGGTGCGCGCTGCCCGCGCG 535  
QY 370 ProArgGlyArgArgArgProAenProSerLysLysProSerArgProArgGlyProGly 389  
DB 536 CCAGAGGTCG 595

QY 390 ArgLeuArgAspLysAlaValProVal 398  
DB 596 CGTCCCCGAGACAAAGCGGTGCCGTG 622

## RESULT 8

LOCUS BE981393/c  
DEFINITION UI-M-CG0p-bdb-f-11-0-UI-s1 NIH\_BMAP\_Ret4\_S2 Mus musculus cDNA clone  
ACCESSION BE981393  
VERSION BE981393.1 GI:10650455  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction; two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
JOURNAL 97044477  
MEDLINE 889548  
PUBMED

## COMMENT

Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: MEST@mail.nih.gov  
Oligo-dT track not found, Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA library Preparation: M.B.  
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA  
clones from RESEARCH GENETICS. It should be noted that Bento Soares  
is generating a small number of additional specialized  
non-redundant arrays of BMAP cDNAs whose availability will be  
considered under appropriate and limited collaborative arrangements  
The tissue for this library was contributed by Dr. Xin-Yuan Fu,  
Yale University School of Medicine  
Seq primer: M13 Forward  
POLYA=No.

## FEATURES

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1..593  
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/db\_xref="taxon:10090"  
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/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; The  
NIH\_BMAP\_Ret4\_S2 library is a subtracted library,  
ultimately derived from mouse retina tissue libraries at  
various stages of development. For a detailed description  
of the library from which this clone was derived, please  
visit our web site at [brainest.eng.uiowa.edu](http://brainest.eng.uiowa.edu). The tissue  
for this library was contributed by Dr. Xin-Yuan Fu, Yale  
University School of Medicine  
TAG\_SEQ=None found"

## ORIGIN

Alignment Scores:  
Pred. No.: 4.74e-58 Length: 593  
Score: 894.00 Matches: 176  
Percent Similarity: 99.44% Conservative: 0  
Best Local Similarity: 99.44% Mismatches: 0  
Query Match: 43.00% Indels: 1  
DB: 2 Gaps: 0

US-09-655-272-2 (1-398) x BE981393 (1-593)

QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20

primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert for range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores: 2,31e-52 Length: 922  
 Pred. No.: 822.50 Matches: 199  
 Score: 822.50 Conserved: 19  
 Percent Similarity: 68.55% Mismatches: 39  
 Best Local Similarity: 62.58% Indels: 62  
 Query Match: 39.56% Gaps: 5  
 DB: 4

US-09-655-272-2 (1-398) x B1758226 (1-922)

1 MetArgSerThrThr-LeuLeuAlaLeuLeuAlaLeuValLeuLeuValSerG1 20  
 134 ATGCGAGCACCACCTGCTCGCTGGCGCTGGTCTTGTCTTACTTGTGTCTGG 193  
 20 yAlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysMetAs 40  
 194 TGCCTCGTGTTCGGGCGCTGGAGAGCCCGCAGCAGCAGCCAGAGGAGCTGG 253  
 40 pHisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAs 60  
 254 GGAGGTCCGAGAGAAGTCTCTGAGGGCCATCGCTGTGTGAGCGACGAGGCTGGCCCT 313  
 60 pPheIleLysLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpTh 80  
 314 CCTCATCAAGGAGGTGGCTGATGCCCTGGGAGGGGGTGGGACCCAGAAACCACTGAC 373  
 80 rAsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyTh 100  
 374 CAGCAACAGCAGCCAC--TCAGCTGGGACCTGGCAGCGCTCTCTTTCTCAGGGAC 430  
 100 rIleIleThrThrIleGlyTyrrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPh 120  
 431 CATCATCACCACTCGCTATGGCATGTGGCGCTCGCTGTTGGGATCTCTTGGCAGGGCTGG 490  
 120 eCysIlePheTyrrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValG1 140  
 491 CTGCACTCTTTATGCTGTGGTGGGATTCGCTGTTGGGATCTCTTGGCAGGGCTGG 550  
 140 yAspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLy 160  
 551 GGACCGGCTGGGCTCTCTCTGCGCATGGCATCGGTCACTTGAAGCATCTTCTT--- 607  
 160 strPhisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuG1 180  
 607 ----- 607  
 180 yCysLeuLeuPheValLeuThrProThrPheValPheSerTyrrMetGluSerTrpSerLy 200  
 607 ----- 607  
 200 sLeuGluAlaIleTyrrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrrVa 220  
 608 -----GTGACGCTTACCACCGTGGCTTGGGCTTGGGCTATGCT 642  
 220 lProGlyAspGlyThrGlyGlnAsnSerProAlaTyrrGlnProLeuValTrpPheTrpI1 240  
 643 GCGCGGCGGACCCCGCAGGAGCTCCCGGCGCTATCAGCGCGCTGGTGTGGTCTGGAT 702  
 240 eLeuPhe-GlyLeuAlaTyrrPheAlaSerValLeuThrThr-IleGlyAsnTrpLeuArg 259  
 703 CCTGCTCGGCGCTGGCTTACTTCCCTCAGTGTCTACCAACCAATCGGAGACTGGCTGCGA 762  
 260 Ala-ValSerArgArgThrArgAla-GluMet-GlyGlyLeuThrAlaGlnAla---Ala 277  
 763 GTAGGTGTGGCGCGCACTCGGGCCAGAGATGGGGCGCGCTCACGGCTTCAGGGCTGCCA 822

554 ATGCGAGCACCACCTGCTGCTGCTGGCAGCTGGTCTTACTTGTGTCTGGG 495  
 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysMetAsp 40  
 494 GCTCTAGTCTTCAGGCTCGGAGCAGCTCAGAGCAGCAGGCTCAGAAGAAATGGAT 435  
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 314 AATAGCAGCAACCACTCATCAGCTTGGAACTCGGCGAGCGCTTCTTTTCTCGGGGACC 255  
 101 IleIleThrThrIleGlyTyrrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 254 ATCATCACTACCTCGCTATGCAATATAGTCTTACACACAGATCGCGGGGCTCTCTTT 195  
 121 CysIlePheTyrrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
 194 TGTATCTTATGACACTGGTGGGATCCCACTGTTCGGGATGCTGCTGGCGGAGTCTGGG 135  
 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 134 GACCGGCTGGGCTCTCTCTGCGCGGGGATCGGCACATCGGCAGCAATCTTCTTGAAG 75  
 161 TrpHisValProGlyLeuValArgSerLeuSer-AlaValLeuPhe 176  
 74 TGGCATGTGCGCAGGCTGCTGAGAAGTGTCTCCCGCAGTCTCTCTTC 26

RESULT 9  
 B1758226  
 LOCUS 603029871F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5200313 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1758226  
 VERSION B1758226.1 GI:15749804  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 922)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Prepared by: The I.M.A.G.E. Consortium (ILNL)  
 cDNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
 http://image.llnl.gov  
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 High quality sequence stop: 785.  
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 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;  
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6  
 male brains, age range 23-27 yo. Library is oligo-dT

FEATURES

source

Qy 278 SerTrpThr---GlyThrValThrAlaArg-ValThrGlnArgThrGlyPro---SerAl 295  
 |||||  
 Db 823 AGCTGGAACCTGGGCACATGTGACAGCGCGCGTGTGACAGCGCGCGCGCGCGC 882  
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RESULT 10  
 AK082153  
 LOCUS  
 DEFINITION  
 Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length  
 enriched library, clone:C230015H11 product:POTASSIUM CHANNEL  
 SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL  
 TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog [Rattus norvegicus],  
 full insert sequence.

ACCESSION  
 AK082153  
 VERSION  
 AK082153.1 GI:26349568  
 KEYWORDS  
 HTC; CAP trapper.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 JOURNAL  
 99279253  
 MEDLINE  
 PUBMED 10349636

REFERENCE  
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 JOURNAL  
 20499374  
 MEDLINE  
 PUBMED 11042159

REFERENCE  
 3 Shino, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Kifunai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 JOURNAL  
 20530913  
 MEDLINE  
 PUBMED 11076861

REFERENCE  
 4 The RIKEN Genome Exploration Research Group Phase II Team and the  
 PANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 JOURNAL  
 20530913  
 MEDLINE  
 PUBMED 11076861

REFERENCE  
 5 The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 JOURNAL  
 20530913  
 MEDLINE  
 PUBMED 11076861

REFERENCE  
 6 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,  
 URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)

COMMENT  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.

URL:http://genome.gsc.riken.jp/  
 URL:http://fantom.gsc.riken.jp/  
 URL:http://location/Qualifiers

#### FEATURES

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1. .2534  
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 VITIGYGNARFSTGGKICFLIYALPGIFLPGLAGDQDLGTFIYGKSIARVEKVF  
 RKQVSQTKRIVSTILFILAGIIVFTVPIVFIKYEIGWALDLSIFVVVTLTVGF  
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#### ORIGIN

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 Query Match: 38.58% Indels: 41  
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US-09-655-272-2 (1-398) x AK082153 (1-2534)

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 Db 303 ATGAAGTGGAAACACAGTGGTGCATCTTCGTGCTGCTGTCTACCTCGTCACTGGT 362  
 Qy 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnAlaGlnLysLysMetAsp 40  
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 Db 363 GGCCTTGTCTTCGCGCCCTTGGAAACAGCCCTTCGAGAGCAGTGCAGAAACACACATCGCC 422  
 Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 |||||  
 Db 423 TTGGAGAGGCGCAGATCTTTGAGAGATCAATCTGTGTGATGCCAGGACTAGACACA 482





Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 99279253  
 10349636  
 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20499374  
 11042159  
 3  
 Kanno, H., Aizawa, K., Katsunai, T., Tashiro, H., Itoh, M.,  
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861  
 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 585-590 (2001)  
 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 2628)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N.,  
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216  
 CDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
 Location/Qualifiers  
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 Query Match: 37.76% Indels: 42  
 DB: 3 Gaps: 11  
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 QY 1 MetArgSerThrLeuLeuAlaLeuAlaLeuValLeuLeuTyrLeuValSerGly 20  
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 QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
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 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLysMetAsp 60  
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 Db 413 CTGATTTCAGCATGCACTCGATGCTAATACCGGGAGTCAGCCAGTA-----CGA 463  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePhePheSerGlyThr 100  
 Db 464 AACTCTCTCAACAGCAGCAGTCACTGGGACCTTGGAGTGGCTCTCTCTTCTGCTGGGACA 523  
 QY 101 IleIleThrThrIleGlyTyrGlyValLeuValLeuHisThrAspAlaGlyArgLeuPhe 120  
 Db 524 GTCATCACAAACCATAGGGTATGGGAATATGTCGCCGACACTGAAGGAGGCAAAATCTTT 583  
 QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
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 QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
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Qy 260 AlaValSerArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaSerTrp 279

Db 1004 GTTTTATCCAAAAGACAAAGAGAGTTGGTGAGATCAAGCCACGCGAGCTGAGTGG 1063

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Qy 291 -----ThrGlyProSerAlaProProGlu----- 299

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Qy 319 AlaGlyArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThr 338

Db 1243 GGACACAGGCGGTT-TCAAGGCTCATCGCAGGAGAGTATCAACA---ACAGACCCCAACA 1298

Qy 339 AlaSerAlaLeu-----AspTyrProSerGluAsnLeuAlaPheIleAspGlu 354

Db 1299 ACCTAGCCTTAAGGGCCGACAGACAGCTTACCAACAATGGCGAGGCGCTTCTGAGGACA 1358

Qy 355 SerSerAspThrGlnSerGluArgGlyCysAlaLeuProArgAlaProArgGlyArg--- 373

Db 1359 ACATCATCAACAGTTTGGGT-----CCACCTCCAACTCACAAAGAGGAAAAACA 1409

Qy 374 -----ArgArgProAsnProSer-----LysLysProSerArgProArgGly 387

Db 1410 AAGATCTCAAAAAGACCTTACCGGAGGATGTCAGAAAAATCTACAAAACCTCCGGA 1466

RESULT 13

AY418067

LOCUS 1113 bp DNA linear GSS 17-DEC-2003

DEFINITION Mus musculus KCN2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY418067

VERSION 1

KEYWORDS GI:39774027

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1113) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

AUTHORS

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1113) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

AUTHORS

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source Location/Qualifiers

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Best Local Similarity: 45.61% Mismatches: 111

Query Match: 37.71% Indels: 23

DB: 9 Gaps: 3

US-09-655-272-2 (1-398) x AY418067 (1-1113)

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Db 1 ATGAATGGAAGACACTCTCCAGATTTCCTGGTGGTCTCTCTACCTGATCATGGGA 60

Qy 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnAlaGlnLysLysMetAsp 40

Db 61 GCACCGTGTTCAGGCAATGGAGCAGCTCAGAGATTTCACAGAGACCACCTTGTG 120

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Db 181 CTCATCCAGCAATAGTGGCAGCAATAAACGCGAGGATTATCCCTC-----TTAGGA 231

Qy 81 AsnSerSerAsnHisSerSerAlaTyrAsnLeuGlySerAlaPhePheSerGlyThr 100

Db 232 ACAGCTCCAAATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTCTTTGCTGGTACT 291

Qy 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120

Db 292 GTTATCACAACTAGATTGGAAACATCTCCCCACGAACTGAAGTGGAAAAATATTC 351

Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140

Db 352 TGCATCATCTATGCTTGTGGGAATTCCTCTTTGGCTTTCTACTGGCTGGGGTGGT 411

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Db 592 CTGGAGCTATCTATTGTTGTTATCTACTGACGACCATTTGGATTGGAGACTACGTG 651

Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240

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Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrIleGlyAsnTrpLeuArgAla 260

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Qy 261 ValSerArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280

Db 772 ATCTCTAAGAAAGACGAAGAGAGTGGGAGAGTTCCAGAGCGCATCCCGCTGAGTGACA 831

Qy 281 GlyThrValThrAlaArgValThrGln-Arg-----Th 291

Db 832 GCCATGTCCGCGCGAGTTCAAGAAACGAGGAGCGGCTGAGCGTGGAGATCTAGCAC 891

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 311 laPro-----ProAlaValValGluProAlaGlyArgProG 323  
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RESULT 14  
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 LOCUS  
 DEFINITION Homo sapiens KNK2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
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 VERSION AY418065.1 GI:39774025  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1113)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarilwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 14671302  
 2 (bases 1 to 1113)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarilwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering them based on alignment.  
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 Score: 778.00  
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 Best Local Similarity: 48.38% Mismatches: 87  
 Query Match: 37.42% Indels: 13  
 DB: 9 Gaps: 3

US-09-655-272-2 (1-398) x AY418065 (1-1113)

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 Db 1 ATGAATGGAGACGGTCTCCAGATATTCCTGGTGGTGTCTCTATCTGATCATCGGA 60  
 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysMetAsp 40  
 Db 61 GCCACCGTGTCAAGCAATGGAGACGCTCATGAGATTTCACAGAGACCAACCATGTG 120  
 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 Db 121 ATCCAGGAAGCAAACTCATATCCCAACATTCCTGTGTCAATTCGAGCGGAGTGGATGA 180

Qy 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyValaAsnProGluThrSerTrpThr 80  
 Db 181 CTATTCAGCAATATGAGGAGCAATTAATGTCAGGAGTATATACCG-----TTAGGA 231  
 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePhePheSerGlyThr 100  
 Db 232 AACACCTCCCAATCAATCAGTCAGTGGAGTTTGGGAAGTTCCTTCTTCTTGTGGCAGCT 291  
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 Db 352 TGTATCATCTATGCTTACTGGGAATTCCTCTTGGTTCCTTCTTGTGGCTGAGTTGA 411  
 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 Db 412 GATCAGCTAGGCACCATATTTGGAAAGAAATTCGCAAGTGGAGATACGTTTATTAAG 471  
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BF565047 469 bp mRNA linear EST 12-DEC-2000  
 LOCUS  
 DEFINITION UI-R-B01-ajm-g-02-0-UI.r1 UI-R-B01 Rattus norvegicus cDNA clone  
 UI-R-B01-ajm-g-02-0-UI 5', mRNA sequence.  
 ACCESSION BF565047  
 VERSION BF565047.1 GI:11674777  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 1 (bases 1 to 469)  
 Bonaldo,M.F., Lemmon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 JOURNAL  
 MEDLINE 97044477  
 PUBMED 8889548

## COMMENT

Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEHRP, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
 clones will be available through Research Genetics (www.resgen.com)  
 This clone is also available through the I.M.A.G.E. Consortium at  
 LLNL (info@image.llnl.gov). IMAGE ID= 1798469  
 Seq primer: M13 Forward.

## FEATURES

Location/Qualifiers

source

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 of the following tissues: thalamus, cerebellum,  
 hypothalamus, medulla, pons, midbrain, cerebral cortex,  
 corpus striatum and hippocampus. For a detailed  
 description of the library from which this clone was  
 derived, please visit our web site at  
 ratseq.eng.uiowa.edu. The subtraction has been previously  
 described in (Bonaldo, Lennon and Soares, Genome Research  
 6:791-806, 1996)"

## ORIGIN

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DB:	2	Gaps:	1

US-09-655-272-2 (1-398) x BF565047 (1-469)

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QY	71	GlyGlyAlaAsnProGluThrSerTrpThrAsnSerSerAsnHisSerSerAlaTrpAsn	90
DB	109	GGGGGGCGCAACCCAGAAACCAAGTTGGACCAATAGCAGCAACCACTCATCAGCTTGGAC	168
QY	91	LeuGlySerAlaPhePheSerGlyThrIleIleThrThrIleGlyTyrGlyAsnIle	110
DB	169	CTGGGACAGCGCCTTCTTTTCTCGGGGACCATCATCACTACCATCGGTACGGCAATATA	228
QY	111	ValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyrAlaLeuValGlyIlePro	130
DB	229	GCCTTACACACAGATCGGGCGTCTCTTTTGTATCTTCATGCACCTGTGGGGATCCCA	288
QY	131	LeuPheGlyMetLeuLeuAlaGlyValGlyAspArgLeuGlySerSerLeuArgArgGly	150
DB	289	CTGTTCGGATGTCTGCTGGAGTCGGGACCGGCTGGGCTCCTCTCTGCGCCGGGC	348
QY	151	IleGlyHisIleGluAlaIlePheLeuLysTrpHisValProProGlyLeuValArgSer	170
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QY	171	LeuSerAlaValLeuPheLeuLeuIleGlyCysLeuLeuPheValLeuThrProThrPhe	190
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 20:30:41 ; Search time 5212.76 Seconds  
(without alignments)  
3356.607 Million cell updates/sec

Title: US-09-655-272-4

Perfect score: 1883

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Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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Database :

GenEmbl.\*

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3: gb.in.\*  
4: gb.om.\*  
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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

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1	1883	100.0	1993	6 AX018706	AX018706 Sequence
2	1883	100.0	1993	6 BD140671	BD140671 Novel mam
3	1870	99.3	1994	6 AK156460	AK156460 Sequence
4	1870	99.3	1994	6 BD228722	BD228722 TREK1-lik

#### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1	AX018706	Sequence 2 from Patent WO945108.	1993 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AX018706	Sequence 2 from Patent WO945108.	1993 bp	DNA	linear	PAT 07-SEP-2000
DEFINITION	AX018706	Sequence 2 from Patent WO945108.	1993 bp	DNA	linear	PAT 07-SEP-2000
ACCESSION	AX018706	Sequence 2 from Patent WO945108.	1993 bp	DNA	linear	PAT 07-SEP-2000
VERSION	AX018706.1	GI:10042827	1993 bp	DNA	linear	PAT 07-SEP-2000
KEYWORDS	AX018706.1	GI:10042827	1993 bp	DNA	linear	PAT 07-SEP-2000
SOURCE	Mus sp.					
ORGANISM	Mus sp.					
REFERENCE	1					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
TITLE	Fink, M., Honore, E., Duprat, F., Lesage, F. and Lazdunski, M.					
JOURNAL	Novel mechanically sensitive mammal potassium channel family activated by polyunsaturated fatty acids and their use particularly for screening medicines					
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DEFINITION	AX018706	Sequence 2 from Patent WO945108.	1993 bp	DNA	linear	PAT 07-SEP-2000
ACCESSION	AX018706	Sequence 2 from Patent WO945108.	1993 bp	DNA	linear	PAT 07-SEP-2000
VERSION	AX018706.1	GI:10042827	1993 bp	DNA	linear	PAT 07-SEP-2000
KEYWORDS	AX018706.1	GI:10042827	1993 bp	DNA	linear	PAT 07-SEP-2000
SOURCE	Mus sp.					
ORGANISM	Mus sp.					
REFERENCE	1					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
TITLE	Fink, M., Honore, E., Duprat, F., Lesage, F. and Lazdunski, M.					
JOURNAL	Novel mechanically sensitive mammal potassium channel family activated by polyunsaturated fatty acids and their use particularly for screening medicines					
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DB: 6 Gaps: 0

US-09-655-272-4 (1-370) x BD140671 (1-1993)

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QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
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QY 281 GlyLeuAlaTyPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
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QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
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DEFINITION Sequence 5 from patent US 6242217.  
ACCESSION AR156460  
VERSION AR156460.1 GI:15125164  
KEYWORDS Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1994)  
AUTHORS Meadows H.Jane. and Chapman,C.Gerald.  
TITLE h-TREK1 polypeptides and h-TREK1 polynucleotides  
JOURNAL Patent: US 6242217-A 5 05-JUN-2001;  
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QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
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Db      1324  GGCTGGCTTACTTTCGAGCTGTTCTGAGCATGATTTGGGACTGGCTACGGGTGATCTCT 1383
Qy      301  LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db      1384  AAGAAGACGAAGAGAGAGTGGGAGAGTTCAGAGCGCATGCCCTGAGTGGACAGCAAT 1443
Qy      321  ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db      1444  GTCACGGCCGAGTTCGAAGGAAACGAGGAGCGCTGAGCGTGAGATCTACGCAAGTTC 1503
Qy      341  GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db      1504  CAGCGTCCCATCCGTGAAGCGGAGAGTCTCCGCGAGAGTGGCGGCAACACACAG 1563
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Db      1564  GAACTGACTCCGTGTATGAGGACC 1587

RESULT 5
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DEFINITION Sequence 5 from Patent WO937762.
ACCESSION AX003051
VERSION    AX003051.1 GI:9926936
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1
AUTHORS    Chapman, C.G. and Meadows, H.J.
TITLE      Trek-1 like two pore potassium channel
JOURNAL    Patent: WO 937762-A 5 29-JUL-1999;
SMITHKLINE BEECHAM PLC (GB)
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Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    99.31%      Indels:      0
DB:             6      Gaps:      0

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Db      664  GAGAGCCCGGTGTTCAAGGATTTGGAGCAGCCTCAGGAGATTTCCCGAGGAGACCACTT 723
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Db      1084  GTTAGTCACAGCAAGATTCGTATCATCTCCACCATCATCTTCATCTGTTTGGCTGTGTC 1143
Qy      221  LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
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Db      1384  AAGAAGACGAAGAGAGTGGGAGAGTTCAGAGCGCATGCCCTGAGTGGACAGCAAT 1443
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Qy      341  GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
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Qy      361  GluLeuThrProCysMetArgThr 368
Db      1564  GAACTGACTCCGTGTATGAGGACC 1587

RESULT 6
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LOCUS      BD273739
DEFINITION Method for identifying anesthetic drug.
ACCESSION    BD273739
VERSION      BD273739.1 GI:33083507
KEYWORDS     JP 2002536017-A/2.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    1
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 3580)
              Lazdunski, M., Honore, E., Lesage, F., Romey, G. and Patel, A.J.
              Method for identifying anesthetic drug

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## ORIGIN

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US-09-655-272-4 (1-370) x MMU73488 (1-3580)

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 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 STRAUSBERG,R.  
 Direct Submission  
 Submitted (13-NOV-2003) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 REMARK  
 COMMENT Contact: MGC help desk

Email: cgabs@mail.nih.gov  
Tissue procurement: Dr. Jim Lin, University of Iowa  
CDNA Library Preparation: M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@cgsc.bc.ca  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
Leticia Hiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline  
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,  
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: WGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 132 Row: P Column: 11  
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/gene="Kcnk2"  
/note="ion trans; Region: Ion transport protein. This  
family contains Sodium, Potassium, Calcium ion channels.  
this family is 6 transmembrane helices in which the last  
two helices flank a loop which determines ion selectivity.  
In some sub-families (e.g. Na channels) the domain is  
repeated four times, whereas in others (e.g. K channels)  
the protein forms as a tetramer in the membrane. A  
bacterial structure of the protein is known for the last  
two helices but is not the Pfam family due to it lacking  
the first four helices"  
/db\_xref="CDD:pfam00520"

# ORIGIN

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Best Local Similarity:			

Query Match:	98.57%	Indels:	0
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DB	25	GTGGCGCCCTGACCTTGGATCCCAAGTCTGCTGCTCAGAACTCCAAACCGAGGCTC	84
QY	21	SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeu	40
DB	85	TCATTCTCTCAAAACCCACCGCTTGTCTCCGGGTGGAGAGTACTCGCCATAAT	144
QY	41	ValMetLysTrpLysThrValSerThrThrPheLeuValValValLeuThrLeuLeu	60
DB	145	GTATGAAATGGAAGACAGCTCTCCAGATTTCTCTGCTGCTGCTCTCTACCTGATCATC	204
QY	61	GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrThrile	80
DB	205	GGAGCCACGGTGTTCAGGCATTGGAGCAGCTTCAGAGATTTCCAGAGGACCACCAT	264
QY	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100
DB	265	GTGATCCAGAGCAGACCTTCATAGCCAGCAGTGCCTGCTCACTCCACCGAGCTGAC	324
QY	101	GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120
DB	325	GAACTCATCCAGCAATAGTGGCAGCAATAAAGCAGGAGTATATCCCTTAGGAAACAGC	384
QY	121	SerAsnGlnValSerHisTAspLeuGlySerSerPhePheAlaGlyThrValIle	140
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QY	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysIle	160
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QY	161	IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln	180
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DB	565	CTAGGAACATATATTTGGAAAGGAATTCGCAAGTGGAAAGACACATTTATTAAGTGAAT	624
QY	201	ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal	220
DB	625	GTTAGTCAGACGAAGATTCGTATCATCTCCACCATCACTTCATCTCTTGGCTGTGTC	684
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QY	261	GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal	280
DB	805	GGATCAGACATGAATATCTGGACTCTACAGCCCTGTGGTGTGTCTTGGATCTCTGTT	864
QY	281	GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer	300
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QY	301	LysLysThrLysGlnValGlyPheArgAlaHisAlaAlaGluTrpThrAlaAsn	320
DB	925	AAGAAGACGAAGAGAGGTGGAGAGTTCAGAGCCATGCCGCTGAGTGGACAGCAAT	984
QY	321	ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe	340
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QY 341 GlnArgAlaThrSerVallySerLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
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LOCUS Rattus norvegicus 2P domain potassium channel KCNK2 mRNA, complete
DEFINITION
cnds.
ACCESSION AF325671
VERSION AF325671.1 GI:15528824
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 3187)
AUTHORS Bockenhauer, D., Zilberberg, N. and Goldstein, S.A.
TITLE KCNK2: reversible conversion of a hippocampal potassium leak into a
voltage-dependent channel
JOURNAL Nat. Neurosci. 4 (5), 486-491 (2001)
MEDLINE 21219399
PUBMED 11319556
REFERENCE 2 (bases 1 to 3187)
AUTHORS Bockenhauer, D. and Goldstein, S.A.N.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-2000) Pediatrics, Section of Developmental
Biology and Biophysics, Yale University Medical School, Boyer
Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
06536, USA

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ORIGIN
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Best Local Similarity: 98.10% Mismatches: 4
Query Match: 97.77% Indels: 0
DB: 10 Gaps: 0

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QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40

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QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80
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Db 329 GTGATCCAGAAACAGAACTTCATAGCCAGCATGCTCGGTCAACTCCACGAGCTGGAT 388
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Db 389 GAACATCATCCAGCAATAGTAGCGGCCATANAATGAGGGATTATCCCTTAGGAACAAC 448
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QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160
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QY 161 IleTrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180
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Thu Feb 3 07:31:03 2005

AF385402 3291 bp mRNA linear ROD 07-MAY-2002  
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 DEFINITION complete cds.  
 ACCESSION AF385402  
 VERSION AF385402.1 GI:19716295  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 3291)  
 Gu, W., Schlachet, G., Hirsch, J.R., Engels, H., Karschin, C.,  
 Karschin, A., Derst, C., Steinlein, O.K. and Daut, J.  
 Expression pattern and functional characteristics of two novel  
 splice variants of the two-pore-domain potassium channel TREK-2  
 J. Physiol. (Lond.) 539 (Pt 3), 657-668 (2002)  
 JOURNAL  
 MEDLINE 21896087  
 PUBMED 11897838  
 REFERENCE 2 (bases 1 to 3291)  
 Derst, C. and Daut, J.  
 Direct Submission  
 Submitted (25-MAY-2001) Lab EEG, Inst. of Human Genetics,  
 Wilhelmstr. 31, Bonn 53111, Germany  
 JOURNAL Location/Qualifiers  
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 ACCESSION AV148474  
 VERSION AV148474.1 GI:23630232  
 KEYWORDS SOURCE  
 ORGANISM Bos taurus (cow)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 1534)



AUTHORS	Enyeart,J.J., Xu,L., Danthi,S. and Enyeart,J.A.
TITLE	An ACTH- and Arp-regulated Background K <sup>+</sup> Channel in Adrenocortical Cells Is TREK-1
JOURNAL	J. Biol. Chem. 277 (51), 49186-49199 (2002)
PUBMED	12368289
REFERENCE	2. (bases 1 to 1534)
AUTHORS	Enyeart,J.J. and Enyeart,J.A.
TITLE	Direct Submission
JOURNAL	Submitted (05-SEP-2002) Neuroscience, The Ohio State University College of Medicine, 5190 Graves Hall, 333 W. 10th Ave, Columbus, OH 43210, USA
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Query Match:	97.50%
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Db	1087 AAAAAAACAAGAAAGAGTGGAGAGTTCAAGCCCCATGCTGCTAGTGGACGCGCCCAAC 1146 
QY	321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrrAspLysPhe 340 
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QY	341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360      :::
Db	1207 CAGCGCGCCACCTCCATTAAAGCGGAAGCTCTCTGAGAACTGGCTGGAAACCAACACAG 1266 
QY	361 GluLeuThrProCysMetArgThr 368 
Db	1267 GAGCTGACTCCCTGTAGGAGGACC 1290 
RESULT 12	
LOCUS	BD273738 1236 bp DNA linear PAT 17-JUL-2003
DEFINITION	Method for identifying anesthetic drug.
ACCESSION	BD273738
VERSION	BD273738.1 GI:33083506
KEYWORDS	JP 2002536017-A/1.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1236) Lazdunski,M., Honore,E., Lesage,F., Romey,G. and Patel,A.J. METHOD FOR IDENTIFYING ANESTHETIC DRUG Patent: JP 2002536017-A 1 29-OCT-2002; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) OS Homo sapiens (human) PN JP 2002536017-A/1 PD 29-OCT-2002 PF 11-FEB-2000 JP 2000598636 PR 12-FEB-1999 US 60/119727.11-FEB-2000 US 09/503089 PI MICHEL LAZDUNSKI,ERIC HONORE, FLORIAN LESAGE, GEORGES ROMEY, PI AMANDA J PATEL



PC C12N15/09.C07K14/47.C12Q1/02.C12Q1/68.G01N33/15.G01N33/50// PC  
(C12Q1/02.C12R1.91).(C12Q1/68.C12R1.91).C12N15/00 CC Nucleic  
acid molecule coding the human TREK-1 channel FH Key

Location/Qualifiers (1)..(1236).  
FT CDS Location/Qualifiers  
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ORIGIN

Alignment Scores:  
Pred. No.: 5,76e-160 Length: 1236  
Score: 1833.00 Matches: 356  
Percent Similarity: 98.91% Conservative: 8  
Best Local Similarity: 96.74% Mismatches: 4  
Query Match: 97.34% Indels: 0  
DB: 6 Gaps: 0

US-09-655-272-4 (1-370) x BD273738 (1-1236)

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Qy 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
Db 61 TCGTTTCCAGAAACCCACACAGTCTTCCCGGTGGAGAGTGACACGACCACTTAAT 120  
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuValLeuIle 60  
Db 121 GTTATGAATGGAAGACCGTCTCCACGATATCTCGTGGTGTTCCTCTATCTGATCATC 180  
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Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
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Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
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Qy 261 GlySerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleLeuVal 280  
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Qy 361 GluLeuThrProCysMetArgThr 368  
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RESULT 13

AF129399 1236 bp mRNA linear PRI 29-MAR-2001  
LOCUS Homo sapiens TREK-1 potassium channel (KCNK2) mRNA, complete cds.  
DEFINITION AF129399  
ACCESSION AF129399.1 GI:5712620  
VERSION AF129399.1  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1236)  
AUTHORS Patel,A.J., Honore,E., Lesage,F., Fink,M., Romey,G. and Lazdunski,M.  
TITLE Inhalational anesthetics activate two-pore-domain background K+ channels  
JOURNAL Nat. Neurosci. 2 (5), 422-426 (1999)  
MEDLINE 99254548  
PUBMED 10321245  
REFERENCE 2 (bases 1 to 1236)  
AUTHORS Patel,A.J., Honore,E., Lesage,F., Fink,M., Romey,G. and Lazdunski,M.  
TITLE Direct Submision  
JOURNAL Submitted (18-FEB-1999) IPCM, CNRS, 660 route des lucioles, Sophia Antipolis, Valbonne 06560, France

FEATURES

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IVALLGTLFGLLAGVGDLGTFGKIAKVEDTIFKNVSGTKIRIITLIFLFG  
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gene

CDS

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ORIGIN

Alignment Scores:

Pred. No.: 5,76e-160 Length: 1236

Score: 1833.00 Matches: 356

Percent Similarity: 98.91% Conservatives: 8

Best Local Similarity: 96.74% Mismatches: 4

Query Match: 97.34% Indels: 0

DB: 9 Gaps: 0

US-09-655-272-4 (1-370) x AF129399 (1-1236)

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DB 1 ATGGCGGCCCTGACTTGGTGGATCTCTAAATCTGCCCTCAGAACTCCAAACCGAGGCTC 60

QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerSerAlaLeuAsn 40

DB 61 TCGTTTTCACGAACCAACAGTCTTCTTCCCGGTGGAGAGTGCACAGCATTAAT 120

QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuLeuLeuLeu 60

DB 121 GTTATGAATGGAAGCGGTCTCCAGATATCTCTGTTCTCTCTATCTGATCATC 180

QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80

DB 181 GGAGCCACCCTGTTCAAGCATTTGGAGCAGCTCATGAGATTTTCACAGAGACCCATT 240

QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHieAlaCysValAenSerThrGluLeuAsp 100

DB 241 GTGATCCAGAAAGCAACATTCATATCCCAACATTTCTGTGTCAATTCGACGAGCTGGAT 300

QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyValSer 120

DB 301 GAATCATTCAGCAATAGTGGAGCATTAATAGGAGGATTAATACGTTAGGAACACC 360

QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140

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DB 541 CTAGGCACCATATTTGGAAAGGAATTCGCAAGTGGAGATACGTTTATTAAGTGGAT 600

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DB 961 GTACAGCCGATTTCAAGAAACACAGAGGCGACTGAGTGTGAGATTTATGACNAGTTC 1020

QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAenHisAenGln 360

DB 1021 CAGCGGCCACCTCCATCAAGCGGAAGCTCTCGCAGAACTGCTGGAAACCAATCAG 1080

QY 361 GluLeuThrProCysMetArgThr 368

DB 1081 GAGCTGACTCTTGTAGGAGACC 1104

RESULT 14

AR156458

LOCUS AR156458 1246 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 1 from patent US 6242217.

ACCESSION AR156458

VERSION AR156458.1 GI:15125162

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1246)

AUTHORS Meadows,H.Jane, and Chapman,C.Gerald.

TITLE h-TREK1 polypeptides and h-TREK1 polynucleotides

JOURNAL Patent: US 6242217-A 1 05-JUN-2001;

FEATURES

Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 5,82e-160 Length: 1246

Score: 1833.00 Matches: 356

Percent Similarity: 98.91% Conservatives: 8

Best Local Similarity: 96.74% Mismatches: 4

Query Match: 97.34% Indels: 0

DB: 6 Gaps: 0

US-09-655-272-4 (1-370) x AR156458 (1-1246)

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DB 69 TCGTTTTCACGAACCAACAGTCTTCTTCCCGGTGGAGAGTGCACAGCATTAAT 128

QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuLeuLeuLeu 60

DB 129 GTTATGAATGGAAGCGGTCTCCAGATATTCCTGTTCTCTCTATCTGATCATC 188

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DB 249 GTGATCCAGAAACCAACATTCATATCCCAACATTTCTGTGTCAATTCGACGAGCTGGAT 308

QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyValSer 120

DB 309 GAATCATTCAGCAATAGTGGAGCAATAAATTCAGGGATTTATACGTTAGGAACACC 368

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1029 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGCAGAACTGGCTGGAAACCAACAATCAG 1088
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Job time : 5229.76 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 20:13:51 ; Search time 566.562 Seconds

(without alignments)  
3428.193 Million cell updates/sec

Title: us-09-655-272-4

Perfect score: 1883

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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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11: Geneseqn2003ds:\*  
12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1870	99.0	1994	2 AAZ00040	Aaz00040 Mouse h-T
3	1864	99.0	3580	3 AAD17497	Aad17497 Murine TR
4	1833	97.3	1236	3 AAD17496	Aad17496 Human TRE
5	1833	97.3	1246	2 AAZ00039	Aaz00039 h-TREK1 p
6	1833	97.3	1246	4 AAC90412	Aac90412 Human TRE

7	1833	97.3	3300	2 AAZ11915	Aaz11915 Human pot
8	1827	97.0	2391	11 ADP03564	Adp03564 Human GPC
9	1805	95.9	2130	4 AAS12169	Aas12169 Human pot
10	1801	95.6	2130	4 AAS12181	Aas12181 Human pot
11	1800	95.6	2130	4 AAS12182	Aas12182 Human pot
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#### ALIGNMENTS

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ID AAZ10607 standard; cDNA; 1993 BP.	
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AC AAZ10607;	
XX	
DT 18-NOV-1999 (first entry)	
XX	
DE cDNA encoding a mechanically sensitive potassium channel protein TREK-1.	
XX	
KW Mechanically sensitive potassium channel protein; TREK-1;	
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;	
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;	
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;	
KW muscular disease; ds.	
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XX	
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PR 05-MAR-1998; 98PR-0002725.	
XX	

(CNRS ) CNRS CENT NAT RECH SCI.  
 Honore E, Fink M, Lazdunski M, Leeage F, Duprat F;  
 WPI; 1999-551038/46.  
 P-PSDB; AAY30648.  
 New mechanically sensitive potassium channel, used to screen for specific modulators, potential therapeutic agents for heart and nervous system disorders.  
 Claim 7; Page 23-25; 40pp; French.  
 The present sequence encodes a mechanically sensitive potassium channel protein designated TREK-1. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with ischemia or anoxia), abnormalities of hormone secretion and muscular disease. The protein itself may be used to treat these diseases. Antibodies specific for the protein are used to detect it in tissues, also as therapeutic inhibitors or activators  
 Sequence 1993 BP; 426 A; 570 C; 561 G; 436 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.58e-213 Length: 1993  
 Score: 1883.00 Matches: 370  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 2  
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 QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 DB 484 ATGGCGGCGCTGACTTGTCTGGATCCCAAGTCTGCTCTAGAACTCCAAACCGAGGCTC 543  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaAlaAsn 40  
 DB 544 TCATCTCTTCAAAACCCACCGTGTCTTCCGGGTGGAGAGTGTACCGCCATTAAAT 603  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60  
 DB 604 GTTATGAATGGAGACAGTCTCCACGATTTCTTGGTGGTCTCTTCTTCTTCTTCTTCT 663  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80  
 DB 664 GGAGCGCGGTGTTCAAGCATTTGAGCAGCTCAGGAGATTTCCAGAGGACCAACCAT 723  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 724 GTGATCCAGAGCAGACACTTATAGCCAGCATGCTCGCTCAACTCCACCGAGCTGGAC 783  
 QY 101 GluLeuIleGlnIleValAlaAlaIleLeuAlaGlyIleIleProLeuGlyAsnSer 120  
 DB 784 GAACATCATCCGAATAGTGGCAGCATTAACCGAGGATTTCCCTTAGGAAACAGC 843  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 DB 844 TCCATCAAGTTAGTACCTGGGACCTCGGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCT 903  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyValIlePheCysIle 160  
 DB 904 ACAACCATAGGATTTGGAACATCTCCACCACTGAGAGTGGAAATATCTGATC 963  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 DB 964 ATCTATGCCTTGTGGGAATTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1023

QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
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 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 DB 1084 GTTAGTCAGACGAGGATTCGTATCATCTCCACCATCATCTTCTTCTTCTTCTTCTTCT 1143  
 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 1144 CTCTTTGTGCTCTCCCTCGGGTCATATTCACGACATAGAGGCTGGAGCGCCCTGGAC 1203  
 QY 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
 DB 1204 GCTATCTATTTTGTGGTTATCACTCTGACGACCATTTGGATTTGGAGACTACGTTGGCAGGT 1263  
 QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
 DB 1264 GGATCAGACATTTGAATATCTGGACTTCTACAGCCTGTGTGTGTGTGTGTGTGTGTGT 1323  
 QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 1324 GGGCTGGCTACTTTGCGAGCTGTTCTGAGCATGATTGGGAGCTGGCTACGGGTGATCTCT 1383  
 QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTyrThrAlaAsn 320  
 DB 1384 AAGAAGACGAAGAGAGGTGGAGAGTTTCAGAGCGCATGCCGCTGAGTGGACAGCCAAAT 1443  
 QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyrAspLysPhe 340  
 DB 1444 GTACGCGCGGATTTCAAGAAACGAGGAGCGGCTGAGCGGTGGAGATCTACGACAGTTC 1503  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 DB 1504 CAGCGTGCACATCCGTGAAGCGGAAGCTCTCCGAGAGCTTCCGAGAGCTGGCGGGCACCACAC 1563  
 QY 361 GluLeuThrProCysMetArgThrCysLeu 370  
 DB 1564 GAACTGACTCCGTGTATGAGGACCTGTCTG 1593  
 RESULT 2  
 AAZ00040  
 ID AAZ00040 standard; DNA; 1994 BP.  
 XX AC AAZ00040;  
 XX 12-OCT-1999 (first entry)  
 XX Mouse h-TREK1 polynucleotide.  
 XX h-TREK1; two pore potassium channel; inflammatory disease;  
 XX chromosome 1q32; ss.  
 XX Mus musculus.  
 XX Key Location/Qualifiers  
 XX CDS 484..1719  
 XX /tag= a  
 XX /product= "h-TREK1"  
 XX WO9937762-A1.  
 XX 29-JUL-1999.  
 XX 02-DEC-1998; 98WO-EP007805.  
 XX 27-JAN-1998; 98EP-00300570.  
 XX 09-OCT-1998; 98GE-00022135.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Meadows HJ, Chapman CG;  
 XX



DR WPI; 1999-469126/39;  
 XX P-PSDB; AAY28497.  
 PT New two pore potassium channel used for, e.g. treatment of cancer,  
 PT pulmonary, cardiovascular and inflammatory diseases.  
 XX Claim 9; Page 25-26; 44pp; English.  
 PS  
 XX This sequence is the h-TREK1 polynucleotide from the mouse, encoding the  
 CC h-TREK1 polypeptide AAY28496. h-TREK1 is a two pore potassium channel.  
 CC The polynucleotide sequence of h-TREK1 can be used to diagnose a disease  
 CC or susceptibility to a disease related to expression or activity of h-  
 CC TREK1 polypeptides. The methods of diagnosis may be used in the treatment  
 CC of diseases including cancer, pulmonary, cardiovascular, and inflammatory  
 CC diseases, pain, psychiatric disorders including depression and  
 CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,  
 CC and head trauma and neurological disorders including migraine  
 XX  
 SQ Sequence 1994 BP; 426 A; 561 C; 561 G; 446 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 5,596-212 Length: 1994  
 Score: 1870.00 Matches: 368  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.31% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-655-272-4 (1-370) x AAZ00040 (1-1994)  
 QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 DB 484 ATGGCGGCCCTGACTTGGTGGATCCCAAGTCTGTCTCAGAACTCCAAACCGAGGCTC 543  
 QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 DB 544 TCATTCCTTTCAAAACCCCGGTGCTTCTCCGGGTGGAGTGAAGTCTGGCCATTAT 603  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIleIle 60  
 DB 604 GTTATGAATGGAAGACAGCTCCACGATTTTCTGTGTGTCTCTACCTGATCATC 663  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
 DB 664 GGAGCCGCGGTGTCAAGCGATTGGAGCAGCCTTCAGAGATTTCACAGAGACCACTT 723  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 724 GTATCCAGAAAGCAGACCTTCATAGCCAGCATGCTGCGTCAACTCCACCGAGCTGGAC 783  
 QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 DB 784 GAATCATCCAGCAATAGTGGCAGCAATAAAGCAGGATTTATCCCTTAGGAACAGC 843  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePhePheAlaGlyThrValIle 140  
 DB 844 TCCAATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTCTTCTGTGTACTGTATC 903  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluClyGlyLysIlePheCysIle 160  
 DB 904 ACAACATAGGATTGGAAACAATCTCCCAAGCACTGAAGGTGGAAATAATTTCTGCATC 963  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 DB 964 ATCTATGCCTTGTGGGAATTCCTCTTTGGTCTTCTACTGCTGGGTGTGTATCAG 1023  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 DB 1024 CTAGGAACATATTTGAAAGGAATTCCTCAAGTGGAGACACATTTATTAGTGAAT 1083  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 DB 1084 GTTAGTCAGACGAAGATTGATATCATCTCCACCATCATCTTCTCTGTGTGTCTGTGTC 1143

QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 1144 CTCTTTGTGGCTCTCCCTGGGTCTATATTCAGAGCATAGAGGCTGGAGCGCCCTGGAC 1203  
 QY 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
 DB 1204 GCTATCTATTTTGTGGTTATCACTCTGACGACCATTTGGATTGGAGACTACGTTGGCAGGT 1263  
 QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
 DB 1264 GATCAGACATTTGAATATCTGACCTCTACAGCCCTGTGTGTGTCTTGGATCCTCGTT 1323  
 QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 1324 GGGCTGGCCCTACTTGTGACGCTGTCTGACGATGATTTGGGAGCTGGCTACGGGTGATCTCT 1383  
 QY 301 LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 DB 1384 AAGAAGACGAAGAGAGAGTGGAGATTTCAGAGCGCATGCCGCTGAGTGGACAGCCAAT 1443  
 QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValIleLysPheLysPhe 340  
 DB 1444 GTACGGCCGAGTTCAAGGAACGAGGAGCGCTGAGGATCTACGACAGATTC 1503  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 DB 1504 CAGCGTGCACATCCGTGAAGCGGAAGCTCTCCGAGAGCTGCGGCGCAACCAACACAG 1563  
 QY 361 GluLeuThrProCysMetArgThr 368  
 DB 1564 GAACGACTCCGTGTATGAGGACC 1587  
 RESULT 3  
 AAD17497  
 ID AAD17497 standard; DNA; 3580 BP.  
 XX AAD17497;  
 DT 10-DEC-2001 (first entry)  
 XX Murine TREK-1 potassium channel protein DNA.  
 DE Murine TREK-1 potassium channel protein DNA.  
 XX Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;  
 KW amnesia; ds.  
 XX Mus musculus.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 484..1719  
 FT /\*tag= a  
 FT /product= "Murine TREK-1 potassium channel protein"  
 PN WO200047738-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-IB0000226.  
 XX  
 PR 12-FEB-1999; 99US-0119727P.  
 PR 11-FEB-2000; 2000US-00503089.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
 XX  
 DR WPI; 2000-549146/50.  
 DR P-PSDB; AAE10342.  
 XX  
 PT Novel nucleic acid encoding a TREK-1 potassium channel protein for  
 PT transfecting cells to be used to identify compounds with anesthetic  
 PT properties.  
 XX

PS Claim 7; Page 29-31; 39pp; English.

XX The invention relates to human and mouse TREK-1 potassium channel  
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
 CC useful for transfecting cells to induce expression of the TREK-1  
 CC potassium channel protein. These cells are then used in assays to  
 CC identify compounds which have anaesthetic properties, producing a safe,  
 CC reversible state of unconsciousness with concurrent amnesia and analgesia  
 CC in a mammal upon inhalation. The present DNA sequence encodes murine TREK  
 CC -1 potassium channel protein

XX Sequence 3580 BP; 870 A; 917 C; 913 G; 880 T; 0 U; 0 Other;

Alignment Scores: 7,07e-211 Length: 3580  
 Pred. No.: 1864.00 Matches: 367  
 Score: 1864.00  
 Percent Similarity: 99.73% Conservative: 0  
 Best Local Similarity: 99.73% Mismatches: 1  
 Query Match: 98.99% Indels: 0  
 Gaps: 0

US-09-655-272-4 (1-370) x AAD17497 (1-3580)

Qy 1 MetAlaLeuProAlaLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 Db 484 ATGGCGGCCCTGACTTGGTGGATCCCAAGTCTGCTCGAATCCCAACCGAGGCTC 543  
 Qy 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 Db 544 TCATTCCTCATAAACCACCGCTGCTTCCCGGGTGGAGAGTGAATCGGCCATTAAAT 603  
 Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIleIle 60  
 Db 604 GTTATGAATGGAAGACAGTCTCCACGATTTCTGGTGGTGGCTTCTACCTGATCATC 663  
 Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
 Db 664 GGAGCGCGGTGTTCAAGSCATTGGAGCAGCTCAGGAGATTTCCAGAGACCCACCAT 723  
 Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 Db 724 GTATCCAGACAGACACCTTCATAGCCAGCATGCTGCGCAACTCCACGAGCTGGAC 793  
 Qy 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 Db 784 GAACTCATCCAGCAATAGTGCACATATAACGAGGAGTATCCCTTAGGAAACAGC 843  
 Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 Db 844 TCCATCAAGTTAGTCACTGGGACCTCGAAGCTCTTTCTTTTGGTGTACTGTATC 903  
 Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 Db 904 ACAACCATAGGATTTGGAACATCTCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 963  
 Qy 161 IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 Db 964 ATCTATGCCCTGCTGGGAATTCCTCTTTTGGCTTTCTACTGCTGGGTTGGTGAATCAG 1023  
 Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 Db 1024 CTAGGAACATATATTGGAAGGAATTTGCCAAGTGAAGACACATTTATTAAGTGAAT 1083  
 Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 Db 1084 GTTAGTCAGACGAGATTCGTATCATCTCCACCATCATCTTCATCTGTTGGCTGTGTC 1143  
 Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 Db 1144 CTCCTTTGGCTCTCCCTGGGTCATATTCAAGACATAGAAGCTGGAGCCCTGGAC 1203  
 Qy 241 AlaIleTyPheValIleIleLeuThrThrIleGlyPheGlyAspTrpValAlaGly 260

Db 1204 GCTATCTATTTTGTGTTATCACTCTGACGACCATGGATTGGAGACTAGTGGCAGGT 1263  
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 Db 1324 GGGCTGGCTCTTTCAGCTGTCTGACCATGATTGGGACTGGCTACGGGTGATCTCT 1383  
 Qy 301 LysLysThrLysGluIleValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 Db 1384 AAGAAGACGGAAGAGAGGTGGAGAGTTTCAGAGCCATGCCGCTGAGTGGACAGCAAT 1443  
 Qy 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyrlsLysPhe 340  
 Db 1444 GTACGCCCGAGTTCAAGGAACAGAGGCGCTGAGCGTGGAGATCTACGACCAAGTTC 1503  
 Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 Db 1504 CAGCGTCCCATCTCCGTGAAGCGGAAGCTCTCCGAGAGCTGGCGGGCAACCAACACAG 1563  
 Qy 361 GluLeuThrProCysMetArgThr 368  
 Db 1564 GAACTGACTCCGTGTAGAGGACC 1587

RESULT 4  
 AAD17496  
 ID AAD17496 standard; DNA; 1236 BP.  
 XX  
 AC AAD17496;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE Human TREK-1 potassium channel protein DNA.  
 XX  
 KW Human; potassium channel protein; TREK-1; anaesthetic; analgesia;  
 XX amnesia; db.  
 OS Homo sapiens.  
 FH  
 FT Key Location/Qualifiers  
 CDS 1..1236  
 FT /\*tag= a  
 FT /product= "Human TREK-1 potassium channel protein"  
 XX  
 PN WO200047738-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-IB000226.  
 XX  
 PR 12-FEB-1999; 99US-0119727P.  
 PR 11-FEB-2000; 2000US-00503089.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 FI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
 DR WPI; 2000-549146/50.  
 DR P-PSDB; AAE10341.  
 XX  
 PT Novel nucleic acid encoding a TREK-1 potassium channel protein for  
 PT transfecting cells to be used to identify compounds with anesthetic  
 PT properties.  
 XX  
 PS Claim 1; Page 26-28; 39pp; English.  
 XX  
 CC The invention relates to human and mouse TREK-1 potassium channel  
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
 CC useful for transfecting cells to induce expression of the TREK-1  
 CC potassium channel protein. These cells are then used in assays to  
 CC identify compounds which have anaesthetic properties, producing a safe,  
 CC identify compounds which have anaesthetic properties, producing a safe,

CC reversible state of unconsciousness with concurrent amnesia and analgesia  
CC in a mammal upon inhalation. The present DNA sequence encodes human TREK-  
CC 1 potassium channel protein

XX Sequence 1236 BP; 330 A; 279 C; 299 G; 328 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 6,92e-208 Length: 1236  
Score: 1833.00 Matches: 356  
Percent Similarity: 98.91% Conservatism: 8  
Best Local Similarity: 96.74% Mismatches: 4  
Query Match: 97.34% Indels: 0  
DB: 3 Gaps: 0

US-09-655-272-4 (1-370) x AAD17496 (1-1236)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
DB 1 ATGGGGCCCTGACTTGGATCTCTGAATCTTAATCTCCGCTCAGAACTCCAAACCGAGCTC 60  
QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
DB 1 TCCTTTTCCACGAAACCCACAGTCTTCTCCGGGTGGAGAGTGACACGACCATTAAT 120  
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuLysLeuIle 60  
DB 121 GTTATGAAATGGAAGACGGTCTCCAGATATCTCGTGGTGTCTCTCTATCTGATCATC 180  
QY 61 GlyAlaAlaValPheLysAlaLeuGluProGlnGluLeuSerGlnArgThrIle 80  
DB 181 GGAGCACCGGTGTCAAGACATTTGGAGCAGCCCTCATGAGATTTCCAGAGGACCCATT 240  
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 241 GTGATCCAGAGCAACATTCATATCCACATCTCTGTGTCAATTCGAGGAGCTGGAT 300  
QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
DB 301 GAATCATTCAGCAAAATAGTGGCAGCAATAAATGACGGGATATACCGTTAGGAACACC 360  
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 361 TCCAAATCAATCAGTCACTGGGATTTGGGAAGTTCTCTCTTCTGTCGACTGTATT 420  
QY 141 ThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160  
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QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
DB 601 GTTAGTCAGACCAAGATTCGCATCATCTCAACATCATATTTATATCTTGGCTGTGTA 660  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
DB 661 CTCTTTGTGGCTCTGCTGCGATCATATTCAAACACATAGAGGCTGGAGTGGCTGGAC 720  
QY 241 AlaIleTyThrValIleThrLeuThrThrIleGlyPheGlyAspThrValAlaGly 260  
DB 721 GCCATTATTATTGGTATTACTCTAAACAACATATTGGATTGGTACACGTTGACGAT 780  
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DB 841 GGGCTTGGCTTACTTGTCTCTGCTGAGCATGATTGGAGATGGCTCCGAGTGATATCT 900  
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QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyAspLysPhe 340  
DB 961 GTCACAGCCGAATTCAAAGAAACACGAGGCGACTGAGTGTGGAGATTATGACAAGTTC 1020  
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
DB 1021 CAGCGGGCCACCTCCATCAAGCGGAGCTCTCGCAGAGACTGCTGGCAAGAACCAATCAG 1080  
QY 361 GluLeuThrProCysMetArgThr 368  
DB 1081 GAGCTGACTCTCTTGTAGGAGGACC 1104  
RESULT 5  
AAZ00039  
ID AAZ00039 standard; DNA; 1246 BP.  
XX AAZ00039;  
AC AAZ00039;  
XX  
DT 12-OCT-1999 (first entry)  
XX  
DE h-TREK1 polynucleotide.  
XX  
KW h-TREK1; two pore potassium channel; inflammatory disease;  
KW chromosome 1q32; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 9..1244  
FT /\*tag= a  
FT /product= "h-TREK1"  
XX  
PN WO9937762-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 02-DEC-1998; 98WO-EP007805.  
XX  
PR 27-JAN-1998; 98EP-00300570.  
PR 09-OCT-1998; 98GB-00022135.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Meadows HJ, Chapman CG;  
XX  
DR WPI: 1999-469126/39.  
DR P-PSDB; AA28496.  
XX  
PT New two pore potassium channel used for, e.g. treatment of cancer,  
PT pulmonary, cardiovascular and inflammatory diseases.  
XX  
PS Claim 9; Page 24; 44pp; English.  
XX  
CC This sequence is the h-TREK1 polynucleotide, encoding the h-TREK1  
CC polypeptide AA28496. h-TREK1 is a two pore potassium channel, and the  
CC gene maps to human chromosome 1q32, between the markers DIS237 and  
CC W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a  
CC disease or susceptibility to a disease related to expression or activity  
CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the  
CC treatment of diseases including cancer, pulmonary, cardiovascular, and  
CC inflammatory diseases, pain, psychiatric disorders including depression  
CC and schizophrenia, neurodegenerative diseases including Alzheimer's,  
CC stroke, and head trauma and neurological disorders including migraine  
XX  
SQ Sequence 1246 BP; 335 A; 280 C; 302 G; 329 T; 0 U; 0 Other;

Alignment Scores:		7.01e-208	Length:	1246
Pred. No.:		1833.00	Matches:	356
Score:		98.91%	Conservative:	8
Percent Similarity:		96.74%	Mismatches:	4
Best Local Similarity:		97.34%	Indels:	0
Query Match:		2	Gaps:	0
DB:				
US-09-655-272-4 (1-370) x AAZ00039 (1-1246)				
Qy	1	MetAlaAlaProhepLeuLeuAppProLysSerAlaAlaGlnAsnSerIysProArgLeu	20	
Db	9	ATGGCGGACCTGACATGCTGGATCTAAATCTGCCGCTCAGAACTCCAAACCGAGGGCTC	68	
Qy	21	SerPheSerSerIysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40	
Db	69	TCGTTTTCACGAACCCACAGTGTCTTCCGGGTGGAGGTGACACGACCAATTAAT	128	
Qy	41	ValMetIysTrpIysThrValSerThrIlePheLeuValValLeuValIleuIle	60	
Db	129	GTATGAATGGAGAGCGTCTCCAGATATCTGCTGGTGTCTCTCTATCTGATCATC	188	
Qy	61	GlyAlaAlaValPheIysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle	80	
Db	189	GGAGCCACCGTGTTCAAAGCATTTGGAGCAGCCTCATGAGATTTTCAGAGGACCACTT	248	
Qy	81	ValIleGlnIysGlnThrPheIleAlaGlnHiEalaCysValAsnSerThrGluLeuAsp	100	
Db	249	GTGATCCAGAACCAACATTCATATCCCAACATTCCTGCTCAATTCGACGAGCTGGAT	308	
Qy	101	GluLeuIleGlnIleValAlaAlaIleAsnAlaGluIleIleProLeuGlyAsnSer	120	
Db	309	GAATCATTCAGCAATAGTGGCAGCAATAAATCAGCGGATTAACCGTTAGGAACACC	368	
Qy	121	SerAsnGlnValSerHisTrpAspLeuGlySerPhePheAlaGlyThrValIle	140	
Db	369	TCCAATCAATCAGTCACTGGGATTTGGAGTTTCTTCTTCTTCTTCTTCTTCTTCTT	428	
Qy	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyIlePheCysIle	160	
Db	429	ACAACCATAGGATTTGGAAACATCTCACCGCAGCAGAGCGGCAAAATATTCGTATC	488	
Qy	161	IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln	180	
Db	489	ATCTATGCTTACTGGGAATTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	548	
Qy	181	LeuGlyThrIlePheGlyIysGlyIleAlaIysValGluAspThrPheIleLysTrpAsn	200	
Db	549	CTAGGCACCATATTTGGAAAGGAATTCGCAAGTGAAGATACGTTTATTAAGTGGAT	608	
Qy	201	ValSerGlnThrIysIleArgIleIleSerThrIleIlePheLeuPheGlyCysVal	220	
Db	609	GTATGTCAGACCAAGATTCGCATCATCTCAACATCATATTTATTAATTTGGCTGTGA	668	
Qy	221	LeuPheValAlaLeuProAlaValIlePheIysHisIleGluGlyTrpSerAlaLeuAsp	240	
Db	669	CTTTTGTGGCTCTGCTCGCATCATATTCACACATAGAGGCTGGAGTGCCTGGAC	728	
Qy	241	AlaIleTyPheValValIleThrLeuThrIleGlyPheGlyAspTyValAlaGly	260	
Db	729	GCCATTTATTTTGTGTTATCACTCAACATTTTGGATTTGGTGACACGTTGCAGGT	788	
Qy	261	GlySerAspIleGluTyLeuAspPheTyLysProValValTrpPheTrpIleLeuVal	280	
Db	789	GGATCCGATATCAATCTGGACCTCTATAGCCCTGCTGCTGCTGCTGCTGCTGCTG	848	
Qy	281	GlyLeuAlaTyPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer	300	
Db	849	GGGCTTGTCTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	908	
Qy	301	LysIysThrIysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn	320	
Db	909	AAAAAGACAAAAGAGGTTGGAGAGTTTCAGAGCACACGCTGCTGCTGCTGCTGCTG	968	
Qy	321	ValThrAlaGluPheIysGluThrArgArgLeuSerValGluIleTyAspIysPhe	340	
Db	969	GTACAGCCGGAATTCAGAGAACACAGAGGACGACTGAGTGTGAGATTTATCACAAGTTC	1028	
Qy	341	GlnArgAlaThrSerValIysArgIysLeuSerAlaGluLeuAlaGlyAsnHisGln	360	
Db	1029	CAGGGGCGACCTCCATCAAGCGGAAGCTCTCGGCAGAACTCGCTGGAAACCAATCAG	1088	
Qy	361	GluLeuThrProCysMetArgThr	368	
Db	1089	GAGCTGACTCTCTTGTAGGAGACC	1112	
RESULT 6				
ID	AAC90412	standard; cDNA; 1246 BP.		
XX	AAC90412;			
XX	19-MAR-2001	(first entry)		
XX	Human TREX coding sequence.			
XX	Human; TREX; 2P domain potassium channel; resting membrane potential;			
XX	neuroal excitability; neurotransmitter release modulation; epilepsy;			
XX	neurological disorder; sleep-related disorder; cognitive dysfunction;			
XX	attention deficit disorder; addition; anxiety; phobia;			
XX	Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;			
XX	erectile dysfunction; alopecia; ss.			
OS	Homo sapiens.			
XX	WO200072863-A2.			
XX	07-DEC-2000.			
XX	01-JUN-2000; 2000WO-GB002107.			
XX	01-JUN-1999; 99GB-00012733.			
XX	(SMIK ) SMITHKLINE BEECHAM PLC.			
XX	Hervieu GJ, Meadows HJ, Randall AD;			
PI	WPI; 2001-080422/09.			
DR	P-PSDB; AAB50044.			
XX	Use of human TREK1 polypeptide, polynucleotides encoding them and			
XX	modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related			
XX	disorders, addition and dyskinesias including Parkinson's and			
XX	Huntington's chorea.			
XX	Claim 12; Page 29; 35pp; English.			
XX	The present sequence is the coding sequence for human TREK1 (h-TREK1). h-			
XX	TREK1 is a member of the 2P domain potassium channel family of proteins			
XX	which play a part in the control of resting membrane potential.			
XX	Modulation of these channels will therefore affect neuronal excitability,			
XX	thereby leading to a modulation of neurotransmitter release and activity			
XX	of neuronal networks. Such modulation therefore may be useful for the			
XX	treatment of certain neurological conditions such as epilepsy, sleep-			
XX	related disorders, cognitive dysfunction, attention deficit disorder,			
XX	addition, anxiety/phobia, Parkinson's and Huntington's chorea, cerebral			
XX	palsy, incontinence, erectile dysfunction or alopecia			
XX	Sequence 1246 BP; 335 A; 280 C; 302 G; 329 T; 0 U; 0 Other;			
Alignment Scores:				
Pred. No.:		7.01e-208	Length:	1246
Score:		1833.00	Matches:	356
Percent Similarity:		98.91%	Conservative:	8
Best Local Similarity:		96.74%	Mismatches:	4
Query Match:		97.34%	Indels:	0

DB:	4	Gaps:	0
US-09-655-272-4 (1-370) x AAC90412 (1-1246)			
QY	1	MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu	20
Db	9	ATGGCGGACCTGACTTGTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC	68
QY	21	SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
Db	69	TCGTTTCCACGAAACCCACAGTGTCTTCCCGGTGGAGAGTGACACGACCATTAAT	128
QY	41	ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle	60
Db	129	GTATGAATGGAAGACGGTCTCCAGATATCTCTGGTGTCTCTATCTGATCATC	188
QY	61	GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle	80
Db	189	GGAGCCACCGTGTCAAGCATTTGGAGCAGCTCATGAGATTTCACAGGAGCACCAT	248
QY	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100
Db	249	GTGATCCAGAAGCAAAATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT	308
QY	101	GluLeuIleGlnGlnIleValAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120
Db	309	GAATCATTTACGAAATAGTGGCAGCAATAAATGCGGGATTATACCGTTAGGAAACACC	368
QY	121	SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle	140
Db	369	TCCAATCAATCAGTCACTGGGATTTGGGAATTCCTTCTTCTGGCATCTGTATT	428
QY	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle	160
Db	429	ACAACCATAGGATTTGGAAACATCTCCACGACACAGAGCGCGCAATAATTCGTATC	488
QY	161	IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln	180
Db	489	ATCTATGCTTACTGGGAATCCCTCTTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG	548
QY	181	LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn	200
Db	549	CTAGGACCCATATTGGAAAGGAATTCGCAAGTGGAGATACGTTTATTAAGTGGAA	608
QY	201	ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal	220
Db	609	GTTAGTCAGACCAAGATTCGCATCATCTCAACAATCATATTTATCTATTTGCTGTGA	668
QY	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp	240
Db	669	CTCTTTTGTGGCTCTGCTGCGATCATATTCAAACACATAGAGGCTGGAGTGCCTGGAC	728
QY	241	AlaIleTyPheValValIleThrLeuThrThrIleGlyPheGlyAspTyValAlaGly	260
Db	729	GCCATTTATTTTGGTATCATCTTAACAACATATTGGATTGGTACATCTGTGAGGT	788
QY	261	GlySerAspIleGluTyLeuAspPheTyLysProValValTrpPheTrpIleLeuVal	280
Db	789	GGATCCGATATGAATATCTGGACTTCTATAAGCCTGCTGCTGGTTCGATCTTGA	848
QY	281	GlyLeuAlaTyPheAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer	300
Db	849	GGGCTTGCTTACTTGTGCTGCTGCTGATGATGATGGATGGCTCCGAGTGATATCT	908
QY	301	LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn	320
Db	909	AAAAAGCAAAAGAGAGTGGAGAGTTCCAGAGCACACCTCTGAGTGACAGGCAAC	968
QY	321	ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyAspLysPhe	340
Db	969	GTACAGCCGAANTTCAAGAAACAGGAGCGGACTGAGTGTGAGATTATGACAAGTTC	1028
QY	341	GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln	360

Db	1029	CAGCGGCGCACCTCCATCAAGCGGAGCTCTCGSCAGAACTGCTGGAAACCAATCAG	1088
QY	361	GluLeuThrProCysMetArgThr	368
Db	1089	GAGCTGACTCTCTTGTAGGAGGACC	1112
RESULT 7			
AAZ11915			
ID	AAZ11915	standard; cDNA; 3300 BP.	
XX	AAZ11915;		
XX	30-NOV-1999	(first entry)	
DE	Human potassium channel K-Hnov59 cDNA.		
XX	Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;		
KW	cardiovascular disorder; CNS disorder; renal disorder; ds.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	CDS	50..1285	
FT		/tag= a	
FT		/product= "Human K-Hnov59 potassium channel"	
XX	WO9943696-A1.		
XX	02-SEP-1999.		
PF	22-FEB-1999;	99WO-US003826.	
XX	25-FEB-1998;	98US-0076687P.	
PR	07-AUG-1998;	98US-0095836P.	
PR	19-JAN-1999;	99US-0116448P.	
XX	(AXYS-) AXYS PHARM INC.		
XX	Miller AP, Curran ME, Hu P, Rutter M, Wang J;		
XX	WPI: 1999-527591/44.		
DR	P-PSDB; AAY34133.		
XX	New nucleic acids encoding mammalian K-Hnov potassium channel proteins,		
PT	useful for the diagnosis and treatment of episodic ataxia with myokymia,		
PT	cardiac arrhythmia, epilepsy and Bartter's syndrome.		
XX	Claim 4; Page 102-104; 112pp; English.		
XX	This sequence represents human potassium channel K-Hnov59 cDNA. K-Hnov		
CC	proteins have a high degree of homology to known potassium channels and		
CC	may be alpha subunits, which form the functional channel, or accessory		
CC	subunits that act to modulate the channel activity. K-Hnov59 is a 4		
CC	transmembrane domain, 2 pore domain potassium channel. The gene is		
CC	located on chromosome 19, determined via PCR chromosomal localisation		
CC	using primers AAZ11939 and AAZ11940. K-Hnov cDNAs were isolated by		
CC	extension of expressed sequence tags (ESTs) which were related but not		
CC	identical to known human potassium channels. Potential polymorphisms		
CC	detected as sequence variants between multiple independent clones.		
CC	Potassium channels have critical roles in various cell types and		
CC	biochemical pathways. Defective potassium channels are known to cause		
CC	four human diseases: episodic ataxia with myokymia; cardiac arrhythmia		
CC	(long QT syndrome); epilepsy; and Bartter's syndrome. As potassium		
CC	channels are critical components of virtually all cells, it is likely		
CC	that abnormal potassium channels are also implicated in certain renal,		
CC	cardiovascular and central nervous system (CNS) disorders. Nucleotides		
CC	encoding K-Hnov proteins may be used for identifying homologous or		
CC	related proteins and the DNA sequences encoding them. They may be used to		
CC	produce compositions that modulate the expression and function of the		
CC	K-Hnov protein and in studying the biochemical pathways associated with		
CC	it. They may also be used for the recombinant production of K-Hnov		
CC	protein in fermentation cultures. Additionally, such nucleotides may be		

used in gene therapy protocols for the treatment of diseases associated with abnormal potassium channels

XX	2200	BB	997	A	629	C	680	G	994	T	0	U	0	Other
CC	2200	BB	997	A	629	C	680	G	994	T	0	U	0	Other

Alignment Scores:	1,09e-207	Length:	3300
Pred. No.:	1833.00	Matches:	356
Score:	98.91%	Conservative:	8
Percent Similarity:	96.74%	Mismatches:	4
Best Local Similarity:	97.34%	Indels:	0
Query Match:	92	Gaps:	0
DB:			

US-09-655-272-4 (1-370) x AAZ11915 (1-3300)

Qy	1	MetAlaIap	ProAspLeuLeuAspProLysSerAlaAlaGlnAenSerLysProArgLeu	20
Db	50	ATGGCGGCACTGACTTGCCTGGATCCTAAATCTGCCGCTCAGAACTCCAACCGAGGCTC	109	
Qy	21	SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn	40	
Db	110	TCGTTTTTCACGAAACCCACAGTGTCTTCCCGGGGAGAGTACACGACCAATTAAT	169	
Qy	41	ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrLeuIleIle	60	
Db	170	GTATATGAATGGAGACGCTCCACGATATTCCTGTGTGTGTCTCTATCTGATCATC	229	
Qy	61	GlyAlaAlaValPheLysAlaLeuGlnProGlnGlnIleSerGlnArgThrThrIle	80	
Db	230	GGAGCCACCGTGTCAAGACATGGAGACGCTCATGAGATTTTCAGAGGACCAACCAT	289	
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100	
Db	290	GTGATCCAGAAGCAACATTCATATCCCAACATTCCTGTGTCATTCGACGGAGCTGGAT	349	
Qy	101	GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120	
Db	350	GAACTCATTCAGCAATATAGGCGAGCAATAAATGACGGATATATACCTTAGGAAACACC	409	
Qy	121	SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle	140	
Db	410	TCCATCAATCAGTCAGTCGGATTTGGGAAGTTCCTCTCTTTGCTTGGCACTGTTATT	469	
Qy	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle	160	
Db	470	ACAACCATAGGATTTGAAACATCTCACACGCACAGAAGCGGCAAAATATTCGTATC	529	
Qy	161	IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln	180	
Db	530	ATCTATGCTTACTGGGAATTCCTCTTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG	589	
Qy	181	LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn	200	
Db	590	CTAGGCACCATATTGGAAAGGAATTTGCCAAAGTGGAAAGATACGTTTATTAAGTGGAA	649	
Qy	201	ValSerGlnThrLysIleArgIleIleSerThrIlePheIleLeuPheGlyCysVal	220	
Db	650	GTATGTCAGACCAAGATTGCACTCATCTCAACATCATATTTATATATTTGGCTGTGTA	709	
Qy	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleLeuGlyTrpSerAlaLeuAsp	240	
Db	710	CTCTTTGTGGCTCTGCCCTGGCATCATATTCAAACACATAGAGCTGGAGTCCCTGGAC	769	
Qy	241	AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly	260	
Db	770	GCCATTTATTTGTGTTATCACTCAACAACTATTGGATTTGGTGCCTACGTTGCAGGT	829	
Qy	261	GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal	280	
Db	830	GGATCCGATATTGAATATCTGACATCTCTATTAAGCCTGTCTGTGGTCTTGGATCTCTGTA	889	
Qy	281	GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer	300	

Db	890	GGGCTTGCTTACCTTGGCTGCTCGTACGATGATGGAGATTGGCTTCCGAGTGATACT	949
Qy	301	LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTyrThrAlaAsn	320
Db	950	AAAAAGACAAAGAGAGTGGGAGAGTTTCAGAGCACACGCTGCTGAGTGGACAGCCAC	1009
Qy	321	ValThrAlaGluPheLysGluThrArgArgLeuSerValGluLeuTyrAspLysPhe	340
Db	1010	GTTCAGCCGCAATTCAAAGAAACAGAGAGCGACTGAGTGTGGAGATTATGACAAGTTC	1069
Qy	341	GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaClyAsnHisAsnGln	360
Db	1070	CAGGGGGCCACCTCCATCAAGCGAAGCTCTCGGCAGAACTGGCTGGAAACCAAAATCAG	1129
Qy	361	GluLeuThrProCysMetArgThr	368
Db	1130	GAGCTGACTCCTTGTAGGAGGACC	1153
RESULT 8			
ADP03564			
ID	ADP03564 standard, DNA; 2391 BP.		
AC	ADP03564;		
CC	29-JUL-2004 (first entry)		
DT	Human GPCR twin pore channel" protein variant "Gene 9" DNA.		
DE	GPCR; G-protein coupled receptor; neuroprotective; nootropic;		
KW	tranquilliser; antimigraine; neuroleptic; antimanic; antidepressant;		
KW	anticonvulsant; antiparkinsonian; cytotatic; cardiac; hypotensive;		
KW	antianal; analgesic; anorectic; anti-HIV; antiaschmatic; osteopathic;		
KW	uropathic; antiulcer; antiallergic; cell cycle regulation; neurological;		
KW	severe mental retardation; dyskinesia; brain; spinal cord; affective;		
KW	neoplastic; cardiovascular; immunological; immune; endocrinal; growth;		
KW	eating; HIV infection; cancer; metabolic; pituitary;		
KW	chromosome identification; gene therapy; human; ds; gene;		
KW	twin pore channel; potassium channel subfamily K member 2 variant.		
OS	Homo sapiens.		
XX	Key		
XX	Location/Qualifiers		
FT	CDS	553..1821	
FT	/*tag= a		
FT	/product= "Human GPCR twin pore channel" protein variant		
FT	"Gene 9" protein"		
FT			
PN	WO2003062393-A2.		
XX			
PD	31-JUL-2003.		
XX			
PF	22-JAN-2003; 2003WO-US001911.		
XX			
PR	22-JAN-2002; 2002US-0350724P.		
XX			
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.		
XX			
PI	Ramanathan CS, Gopal S, Mintier G, Feder JN;		
XX			
DR	WPI; 2003-618283/58.		
DR	P-PSDB; ADP03575.		
XX			
PT	New nucleic acid molecule encoding a human G-protein coupled receptor,		
PT	useful for diagnosing, preventing or treating diseases involving the		
PT	receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or		
PT	cancer.		
XX			
PS	Claim 1; SEQ ID NO 9; 224pp; English.		
XX			
CC	The invention relates to a novel isolated GPCR (G-protein coupled		
CC	receptor) nucleic acid molecule. The polynucleotide and polypeptide of		
CC	the invention demonstrate neuroprotective, nootropic, tranquilliser,		
CC	antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,		

CC antiparkinsonian, cytostatic, cardiant, hypotensive, antianginal,  
 CC analgesic, anorectic, anti-HIV, antiaesthetic, osteopathic, uropathic,  
 CC antiulcer and anti-allergic properties. The nucleic acid molecule and  
 CC polypeptide of the invention may be useful in diagnosing, preventing,  
 CC treating or ameliorating a medical condition, such as a disorder related  
 CC to aberrant G-protein coupled signalling, a disorder related to aberrant  
 CC cell cycle regulation, neurological disorders, severe mental retardation  
 CC and dyskinesias, brain disorders, spinal cord disorders, affective  
 CC disorders, neoplastic disorders, cardiovascular disorders, immunological  
 CC disorders, immune-related disorders, endocrinal diseases, growth  
 CC disorders, eating disorders, HIV infection, cancers, metabolic disorders  
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in  
 CC chromosome identification, in identifying organisms from minute  
 CC biological samples, in gene therapy or as a molecular weight marker. The  
 CC current sequence is that of a human GPCR (G-protein coupled receptor) DNA  
 CC which was isolated by the method of the invention.

SQ Sequence 2391 BP; 662 A; 503 C; 537 G; 689 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 9.81e-207 Length: 2391  
 Score: 1827.00 Matches: 354  
 Percent Similarity: 98.91% Conservative: 10  
 Best Local Similarity: 96.20% Mismatches: 4  
 Query Match: 97.03% Indels: 0  
 DB: 11 Gaps: 0

US-09-655-272-4 (1-370) x ADP03564 (1-2391)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 DB 586 TTGGCGGCACCTGACTTGGTGGATCTCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 645  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 DB 646 TCGTTTCCACGAAACCCACAGTGTCTTCCGGGTGGAGTGNACAGACCACTTAT 705  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60  
 DB 706 GTTATGAATGGAAGACGGTCTCCACGATATCTCGTGGTGTCTCTATCTGATCATC 765  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80  
 DB 766 GGAGCCACCGTGTTCAAAGCATTTGGAGCAGCCCTCATGAGATTTTCACAGAGCACCAT 825  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 826 GTGATCCAGAGCAACATTCATATCCACATCTCTGTCTCAATTCGACGGAGCTGGAT 885  
 QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 DB 886 GAACTCATTGAGCAATAGTGGCAGCAATAAATGCAGGGATTATACCGTTAGGAAACACC 945  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 DB 946 TCCAAATCAATAGTACATCGGATTTGGGAAGTTCCTTCTTCTGTCGCACTGTATT 1005  
 QY 141 ThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 DB 1006 ACACCATAGGATTTGGAAACATCTCACACGACACAGAGCGGCAAAATATCTGTATC 1065  
 QY 161 IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 DB 1066 ATCTATGCCCTTACTGGGAATCCCTCTTTGGTCTTCTTGGCTGGAGTTGGAGATCAG 1125  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 DB 1126 CTAGGCACCATATTTGGAAAGGAATTCGCAAGTGGAAAGATACGTTTATTAAGTGAAT 1185  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 DB 1186 GTTAGTCAGACCAAGATTCGATCATCTCAACATCATATTTTACTATTGTGGCTGTGTA 1245

QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 1246 CTCCTTTGTGGCTCTGCTGCGATCATATTCAAACACATAGAGGCTGGAGTGCCTGGAC 1305  
 QY 241 AlaIleTyPheValValIleThrLeuThrThrIleGlyPheGlyAspTyValAlaGly 260  
 DB 1306 GCCATTTATTTTGGTTTATCACTCTAACACTATTGGATTGGTGTGACTACGTTCAGGT 1365  
 QY 261 GlySerAspIleGluTyTrpLeuAspPheTyTrpLysProValValTrpPheTrpIleLeuVal 280  
 DB 1366 GGATCCGATATTGAATATCTGGACTTCTATAAGCCCTGCTGTGGTTCCTGATCCTTGTA 1425  
 QY 281 GlyLeuAlaTyPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 1426 GGGCTTGTCTTACTTTCCTGCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 1485  
 QY 301 LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTyrThrAlaAsn 320  
 DB 1486 AAAAAACAAGAGAGAGGTGGAGAGTTCAAAAGCACGCTGCTGAGTGGACAGCCAAC 1545  
 QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyAspLysPhe 340  
 DB 1546 GTCACAGCCGATTTCAAGAAACACAGGAGCGGACTGAGTGTGGAGATTTATGACAAAGTTC 1605  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 DB 1606 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGCAGAACTGCTGGAAACCAACATCAG 1665  
 QY 361 GluLeuThrProCysMetArgThr 368  
 DB 1666 GAGCTGACTCTTGTAGGAGGACC 1689  
 RESULT 9  
 AAS12169  
 ID AAS12169 standard; cDNA; 2130 BP.  
 XX AAS12169;  
 AC AAS12169;  
 DT 21-NOV-2001 (first entry)  
 XX Human potassium ion channel TPKC1 cDNA.  
 DE Transmembrane potassium ion channel protein; inward potassium flux; ss;  
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
 XX insect; TPKC1; human.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 178..1458  
 FT /\*tag= a  
 FT /product= "Human TPKC1 protein"  
 XX  
 PN WO200161006-A2.  
 XX  
 XX 23-AUG-2001.  
 XX  
 XX 14-FEB-2001; 2001WO-US004680.  
 XX  
 XX 15-FEB-2000; 2000US-00503849.  
 XX  
 XX (BADI ) BASF CORP.  
 XX PA  
 XX Pausch MH;  
 XX  
 XX WPI; 2001-536570/59.  
 XX P-PSDB; AAU07618.  
 XX  
 XX New polypeptide, a mutant potassium ion channel protein for improving  
 XX inward potassium flux under acidic conditions.  
 XX  
 XX Example 15; Page 45-46; 131pp; English.  
 XX



CC The invention relates to a mutant potassium ion channel protein, having a  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human cDNA encoding a transmembrane potassium ion channel  
 CC protein, TPCK1  
 XX  
 SQ Sequence 2130 BP; 564 A; 480 C; 488 G; 593 T; 0 U; 5 Other;

Alignment Scores:  
 Pred. No.: 3,44e-204 Length: 2130  
 Score: 1805.00 Matches: 352  
 Percent Similarity: 98.37% Conservative: 10  
 Best Local Similarity: 95.65% Mismatches: 6  
 Query Match: 95.86% Indels: 0  
 DB: 4 Gaps: 0

US-09-655-272-4 (1-370) x AAS12169 (1-2130)

QY 1 MetAlaLaProAspLeuLeuAspProLysSerAlaGlnAsnSerLysProArgLeu 20  
 DB 223 GTGGCGGCACCTGCTGCTGATCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 282  
 QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 DB 283 TCATTTTCCAGAAACCCACAGTGTCTGCTTCCGGGTGGAGTGCACAGCACCATTAT 342  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuThrLeuIle 60  
 DB 343 GTTATGAATGGAAGACGGTCTCCACGATATCTCGTGTGGTGTCTCTATCTGATCATC 402  
 QY 61 GlyAlaAlaValPheLysAlaLeuGlnProGlnGluLeuSerGlnArgThrIle 80  
 DB 403 GGAGCCACCGTGTTCAGAGCATGGAGCAGCTCATGAGATTCACAGAGCACCATT 462  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 463 GTGATCCAGAGCAACATTCATATCCCAACATTCCTGTCAATTCAGCGAGCTGGAT 522  
 QY 101 GluLeuIleGlnGlnIleValAlaAlaLeuAlaGlyIleIleProLeuGlyAsnSer 120  
 DB 523 GAACATCATTCAGCAATAGTGGCAGCAATAAATGAGGAGTATACCTTTAGGAAACACC 582  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValle 140  
 DB 583 TCCAAATCAATCAGTCACTGGGATTTGGGAGTTCCTTCTTCTTGTGGCAGCTGTATT 642  
 QY 141 ThrThrIleGlyPheGlyAsnLeuSerProArgThrGluGlyGlyIlePheCysIle 160  
 DB 643 ACAACCATAGGATTTGGAAACATCTCACACGACAGAGCGGCAAAATATCTGTATC 702  
 QY 161 IleTyraLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180  
 DB 703 ATCTATGCCCTTACTGGGAATTCCTTCTTGTGTTTCTTGTGGTGGAGTTGAGATCAG 762  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 DB 763 CTAGGCACCATATTTGGAAAGGAATTCGCAAGTGGAAAGATACGTTTAAAGTGGAAAT 822  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 DB 823 GTTAGTCAGACCAAGATTCGATCATCTCAACATCATATTTATATATTGGCTGTGTA 882  
 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 883 CTCCTTTGGTCTTGGCTGGATCATATTCAAACACATAGAGGCTGGAGTGCCTGGAC 942

QY 241 AlaIleTyraPheValValIleThrLeuThrThrIleGlyPheGlyAspTyraValAlaGly 260  
 DB 943 GCCATTTATTTTGTGTATCACTCTAAACAATTTGGATTTGGTACTACGTTGCAGGT 1002  
 QY 261 GlySerAspIleGluTyraLeuAspPheTyraLysProValValTrpPheTrpIleLeuVal 280  
 DB 1003 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGTCTGTGTGTCTGGATCCTTGA 1062  
 QY 281 GlyLeuAlaTyraPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 1063 GGGCTTCTTACTTTGTCTGTCTCTGAGCATATTTGGGAGATTGTCGAGTGTATCT 1122  
 QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaGlnTrpThrAlaAsn 320  
 DB 1123 AAAAAGACAAAAGAGAGTGGGAGATTTCAGAGCACGCTCTGAGTGAGCAGCAAC 1182  
 QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyraAspLysPhe 340  
 DB 1183 GTCACGCGGAATTCAAAGAAACCCAGGAGGCGTGTGTGTGGAGATTTATGACAAGTTC 1242  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisGln 360  
 DB 1243 CAGCGGCCACCTCATCAAGCGGAAGCTCTCGGACAGACTGGCTGGAAACCAATCAG 1302  
 QY 361 GluLeuThrProCysMetArgThr 368  
 DB 1303 GAGCTGACTCTTGTAGGAGACC 1326  
 RESULT 10  
 AAS12181  
 ID AAS12181 standard; cDNA; 2130 BP.  
 XX  
 AC AAS12181;  
 XX 21-NOV-2001 (first entry)  
 DT Human potassium ion channel protein TPCK1 cDNA mutant #1.  
 DE Transmembrane potassium ion channel protein; inward potassium flux; ss;  
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
 KW insect; TPCK1; human; mutant.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 CDS 178..1458  
 FT /\*tag= a  
 FT /product= "Human TPCK1 mutant protein #1"  
 FT mutation replace(943,G)  
 FT /\*tag= b  
 XX WO200161006-A2.  
 PN 23-AUG-2001.  
 XX 14-FEB-2001; 2001WO-US0004680.  
 PF 15-FEB-2000; 2000US-00503849.  
 PR (BADI ) BASF CORP.  
 XX Pausch MH;  
 PI WPI; 2001-536570/59.  
 DR P-PSDB; RAU07622.  
 XX New polypeptide, a mutant potassium ion channel protein for improving  
 PT inward potassium flux under acidic conditions.  
 XX Claim 12; Page 121-122; 131pp; English.  
 PS The invention relates to a mutant potassium ion channel protein, having a  
 CC four membrane spanning domains and two pore forming domains, comprising a

Qy 241 AlaIleTyrPheValValIleThrIleuThrThrIleGlyPheGlyAspTyrValAlaGly 260

CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human cDNA encoding a transmembrane potassium ion channel  
 CC mutant TPKC1 protein  
 XX Sequence 2130 BP; 564 A; 481 C; 488 G; 592 T; 0 U; 5 Other;  
 SQ

Alignment Scores: 1.36e-203 Length: 2130  
 Pred. No.: 1800.00 Matches: 351  
 Score: 98.37% Conservative: 11  
 Percent Similarity: 95.38% Mismatches: 6  
 Best Local Similarity: 95.59% Indels: 0  
 Query Match: 4 Gaps: 0  
 DB:

US-09-655-272-4 (1-370) x AAS12182 (1-2130)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAenSerLysProArgLeu 20  
 Db 223 GTGGGGGACCTGACTGCTGATCTTAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 282  
 QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerSerAlaIleAsn 40  
 Db 283 TCATTTTCCAGAAACCCACACAGTCTTGCCTCCCGGTGGAGAGTGACAGACANTTAT 342  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuLysLeuIle 60  
 Db 343 GTTATGAATGGAGACGGTCTCCAGCATATCTCTGGTGTGCTCTATCTGATCATC 402  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80  
 Db 403 GGAGCCACCGTGTTCAGAGCATGGAGCAGCTCATGAGATTTCCAGAGGACCCACAT 462  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 Db 463 GTGATCCAGAGCAAAACATTCATATCCCAACATTCCTGTGTCAATTCAGCGAGCTGAT 522  
 QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 Db 523 GAATCATTCAGCAATAGTGGCAGCAATAAATGCGGATATATACCGTTAGGAAACAC 582  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 Db 583 TCCATCAATCAGTCACCTGGGATTTGGGAAGTTCCTTCTTCTTCTGGCAGCTGTATT 642  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyIlePheCysIle 160  
 Db 643 ACAACCATAGGATTTGGAAACATCTCACCGCAGAGAGGGCGCAAAATATTTCTGTATC 702  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValClyAspGln 180  
 Db 703 ATCTATGCTTACTGGGAATTCCTCTTTTGTGTTTCTCTGGCTGGAGTTGGAGATCAG 762  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 Db 763 CTAGGACCATATTTGGAAAGGATTTGCCAAGTGGAGAGATACGTTTATTAAGTGAAT 822  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheLeuPheGlyCysVal 220  
 Db 823 GTTAGTCAGACCAAGATTCGATCATCTCAACATCATATTTATATTTTGGCTGTGTA 882  
 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 Db 883 CTCTTTTGGCTCTGCTGCGATCATATTCAAACATAGAGGCTGGAGTCCCTGGAC 942  
 QY 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
 Db 943 GCCATTATTTTGGTGTATCACTCTTAACAACATTTGGATTGGTGGTGGTGGTGGT 1002

QY 261 GlySerAspIleGluTyrIleuAspPheTyrLysProValValTrpPheTrpIleuVal 280  
 Db 1003 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGCTGTTGGTTCCTTGA 1062  
 QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 Db 1063 GGGCTTCTTACTTGTCTGCTGCTGAGCATATTTGGAGATTGGTCCGAGTGATATCT 1122  
 QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 Db 1123 AAAAGAACAAAGAGAGGTTGGAGATTTCAGAGCACACGCTGCTGAGTGGACAGCAAC 1182  
 QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyrAspLysPhe 340  
 Db 1183 GTACAGCCGAATTCAAAGAAACCCAGAGGCGACTGAGTGTGGAGATTATGACAAAGTTC 1242  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 Db 1243 CAGCGGGCCACCTCCATCAACGGAGAGCTCTGGCAGAACTGGCTGGAAACCAACATCAG 1302  
 QY 361 GluLeuThrProCysMetArgThr 368  
 Db 1303 GAGCTGACTCTTGTAGGAGGACC 1326  
 RESULT 12  
 AAS12184  
 ID AAS12184 standard; cDNA; 2130 BP.  
 XX AAS12184;  
 AC AAS12184;  
 XX 21-NOV-2001 (first entry)  
 DT Human potassium ion channel protein TPKC1 cDNA mutant #4.  
 DE Transmembrane potassium ion channel protein; inward potassium flux; ss;  
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
 KW insect; TPKC1; human; mutant.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 PH CDS 178..1458  
 FT /\*tag= a  
 FT /product= "Human TPKC1 mutant protein #4"  
 FT mutation replace(985,G)  
 FT /\*tag= b  
 FT WO200161006-A2.  
 XX 23-AUG-2001.  
 XX 14-FEB-2001; 2001WO-US0004680.  
 XX 15-FEB-2000; 2000US-00503849.  
 XX (BADI ) BASF CORP.  
 XX Pausch MH;  
 FI WPI; 2001-536570/59.  
 DR P-PSDB; AAU07625.  
 DR New polypeptide, a mutant potassium ion channel protein for improving  
 PT inward potassium flux under acidic conditions.  
 XX Claim 12; Page 126-127; 131pp; English.  
 PS The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve





XX PS Claim 2; SEQ ID NO 346; 591pp; English.

XX CC The invention relates to novel human diagnostic and therapeutic

CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded

CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to

CC polynucleotide sequences at least 90% identical to the dithp cDNA

CC sequences of the invention; recombinant vectors, host cells and

CC transgenic organisms comprising a dithp nucleic acid sequence; the

CC recombinant production of DITHP proteins; antibodies specific for DITHP

CC proteins; microarrays comprising dithp nucleic acid sequences; methods of

CC detecting dithp nucleotide and protein sequences; methods of screening

CC for compounds which specifically bind a DITHP protein; and methods of

CC assessing the toxicity of test compounds using a dithp hybridisation

CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the

CC diagnosis of a wide variety of conditions including cancer and other cell

CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,

CC viral, fungal or parasitic infections; hormonal disorders; metabolic

CC disorders; neurological disorders; gastrointestinal disorders; transport

CC disorders; and connective tissue disorders. They may also be used to

CC screen for modulators of protein activity or gene expression. DITHP

CC proteins can additionally be used in analysis of the proteome of a tissue

CC or cell type and to induce antibodies. The dithp nucleic acids are

CC additionally useful in somatic or germline gene therapy of the disorders

CC mentioned above, as a source of antisense sequences, as a source of

CC probes and primers, in genotyping and identification of individuals, in

CC the generation of transgenic animal models of human disease or knock in

CC humanised animals, in toxicological testing, and in transcript imaging.

CC The present sequence represents a dithp cDNA encoding a DITHP protein

CC which has membrane transport protein activity. Note: The sequence data

CC for this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 3393 BP; 978 A; 667 C; 716 G; 1032 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.49e-196 Length: 3393

Score: 1743.50 Matches: 351

Percent Similarity: 97.83% Conservative: 9

Best Local Similarity: 95.38% Mismatches: 8

Query Match: 92.59% Indels: 4

DB: 8 Gaps: 0

US-09-655-272-4 (1-370) x ACC46425 (1-3393)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20

DB 188 GTGGGGGACCTGACTTGTGGATCTTAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 247

QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40

DB 248 TCATTTTCCAGAAACCCACAGCTGTCTTCCCGGTGGAGAGTGACACGACCAATTAAT 307

QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuTrpIleIleIle 60

DB 308 GTTATGAAATGGAAGACGGTCTCCAGATATTCTCTGGTGTCTCTATCTGATCATC 367

QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80

DB 368 GGAGGCCCGTGTTCAAAGCATTTGGAGCAGCTTCATGAGATTTTCAGAGGACCACTT- 426

QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100

DB 427 GTGATCCAGAGCA-ACATTCATATCCCA-CATTCTCTGTGTCTAT-TCGACGGAGCTGGAT 483

QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120

DB 484 GAACTCATTCAGCAATAGTGGCAGCAATAAATGAGGGATTATACCGTTAGGAAACACC 543

QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140

DB 544 TCCAAATCAATCAGTCAGTGGGATTTGGGAAGTTCTCTTCTTGTGGCACTGTATT 603

QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160

DB 604 ACAACCATAGGATTTGGAAACATCTCACACGACAGAGGGCGGCAAAATATTCTGTATC 663

QY 161 IleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180

DB 664 ATCTATGCTTACTGGGAATTCCTCTTGTGTTTCTCTGCTGGAGTTGGAGATCAG 723

QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200

DB 724 CTAGGCACCATATTGGAAAGGAATTCGCAAGTGAAGATACGTTTATTAAAGTGAAT 763

QY 201 ValSerGlnThrLysIleIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220

DB 784 GTTAGTCAGACCAAGATTGCGATCATCTCAACAATCATATTTATATTATTTGGCTGTGA 843

QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240

DB 844 CTCCTTGTGGCTCTGCTGCGATCATATTCAACACATAGAAGCTGGAGTGCCTGGAC 903

QY 241 AlaIleTrpPheValIleThrLeuThrIleGlyPheGlyAspTrpValAlaGly 260

DB 904 GCCATTATTTTGTGTTATCACTCTAACAACTATTGGATTGGTGACTACGTTGCAGGT 963

QY 261 GlySerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleLeuVal 280

DB 964 GGATCCGATATTGAATATCTGACACTCTATAAGCCTGCTGCTGGTTCCTGGATCCTTGA 1023

QY 281 GlyLeuAlaTrpPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300

DB 1024 GGGCTGTGCTTACTTGTGCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 1083

QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320

DB 1084 AAAAGACAAAAGAGAGGTGGAGATTTCAGACACACGCTGCTGAGTGGACGCCAAC 1143

QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTrpAspLysPhe 340

DB 1144 GTCACAGCCGATTTCAAAGAAACACGAGGCGACTGAGTGTGAGATTATGACAAATTC 1203

QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyHisAsnGln 360

DB 1204 CAGCGGGCCACTCCATCAAGCGGAAGCTCTCGGCAGAACTGGCTGGAACCAATCAG 1263

QY 361 GluLeuThrProCysMetArgThr 368

DB 1264 GAGCTGACTCTCTTAGGAGGACC 1287

RESULT 15

ADJ27238

ID ADJ27238 standard; DNA; 1702 BP.

XX AC ADJ27238;

XX DT 20-MAY-2004 (first entry)

XX DE Human TRICH-22 coding sequence, SEQ ID 70.

XX KW Human; Transporters and Ion Channels protein; TRICH; Transporter;

KW Ion Channel; transport disorder; neurological disorder; muscle disorder;

KW Immunological disorder; cell proliferative disorder; infection;

KW Neuroprotective; Muscular; Respiratory; Antidiabetic; Antiparkinsonian;

KW Nootropic; Anticonvulsant; Antithyroid; Ophthalmological; Antibacterial;

KW Antiinflammatory; Cardiant; Anti-anginal; Antiarrhythmic; Antiasthmatic;

KW Endocrine; Hypotensive; Anti-HIV; Antianemic; Antiarteriosclerotic;

KW Dermatological; Antiarthritic; Osteopathic; Antipsoriatic; Antirheumatic;

KW Immunosuppressive; Anticancer; Gastrointestinal; Hepatotrophic; Cystostatic;

KW Virucide; Fungicide; Antiparasitic; Protozoacide; Antihelminthic;

KW Gene Therapy; TRICH-22; gene; ds.

XX OS Homo sapiens.

XX XX

Search completed: February 2, 2005, 22:33:24  
Job time : 582.562 secs

Search completed: February 2, 2005, 22:33:24  
Job time : 582.562 secs



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 22:01:01 ; Search time 99.7266 Seconds  
(without alignments)  
2637.130 Million cell updates/sec

Title: US-09-655-272-4

Perfect score: 1883

Sequence: 1 MAAPDLLDPKSAQNSKPL.....SALAGNHQELTPCMTCL 370

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*  
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4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1870	99.3	1994	3	US-09-236-080-5
2	1833	97.3	1246	3	US-09-236-080-1
3	1833	97.3	3300	3	US-09-336-643A-82
4	1247.5	66.3	2730	4	US-09-799-451-432
5	797	42.3	1182	4	US-09-432-470-1
6	797	42.3	1218	4	US-09-432-470-3
7	797	42.3	3996	4	US-09-620-312D-195
8	547	29.0	321	3	US-09-236-080-3
9	416.5	22.1	1497	4	US-09-561-763-3
10	416.5	22.1	1497	4	US-09-431-367B-3
11	416.5	22.1	3452	4	US-09-561-763-1
12	416.5	22.1	3452	4	US-09-431-367B-1

13	397.5	21.1	1086	4	US-09-362-842-13	Sequence 13, Appl
14	387	20.6	996	4	US-09-561-763-6	Sequence 6, Appl
15	387	20.6	996	4	US-09-431-367B-6	Sequence 6, Appl
16	387	20.6	1575	4	US-09-561-763-4	Sequence 4, Appl
17	387	20.6	1575	4	US-09-431-367B-4	Sequence 4, Appl
18	378.5	20.1	2514	3	US-09-144-914-3	Sequence 3, Appl
19	377	20.0	1882	4	US-09-814-915A-45	Sequence 45, Appl
20	377	20.0	1894	3	US-08-749-816-1	Sequence 1, Appl
21	377	20.0	1894	3	US-09-144-914-1	Sequence 1, Appl
22	342	18.2	939	4	US-09-561-763-9	Sequence 9, Appl
23	342	18.2	939	4	US-09-431-367B-9	Sequence 9, Appl
24	342	18.2	2287	4	US-09-561-763-7	Sequence 7, Appl
25	342	18.2	2287	4	US-09-431-367B-7	Sequence 7, Appl
26	342	18.2	2571	3	US-09-336-643A-80	Sequence 80, Appl
27	317.5	16.9	1227	4	US-09-362-842-11	Sequence 11, Appl
28	315	16.7	2441	1	US-08-332-312-1	Sequence 1, Appl
29	256.5	13.6	1188	4	US-09-362-842-5	Sequence 5, Appl
30	219	11.6	1011	1	US-08-332-312-3	Sequence 3, Appl
31	216.5	11.5	2193	4	US-09-362-842-3	Sequence 3, Appl
32	212	11.3	1203	4	US-09-561-763-12	Sequence 12, Appl
33	212	11.3	1203	4	US-09-431-367B-12	Sequence 12, Appl
34	212	11.3	1506	4	US-09-561-763-10	Sequence 10, Appl
35	212	11.3	1506	4	US-09-431-367B-10	Sequence 10, Appl
36	211	11.2	2288	4	US-09-362-842-1	Sequence 1, Appl
C 37	203.5	10.8	3033	4	US-09-362-842-66	Sequence 66, Appl
C 38	203.5	10.8	3033	4	US-09-270-767-13872	Sequence 13872, A
C 39	174.5	9.3	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 40	174.5	9.3	1664976	4	US-09-692-570-1	Sequence 1, Appl
41	172	9.1	3462	4	US-09-362-842-7	Sequence 7, Appl
42	162.5	8.6	923	3	US-09-336-643A-15	Sequence 15, Appl
C 43	141	7.5	438	4	US-09-362-842-68	Sequence 68, Appl
C 44	141	7.5	438	4	US-09-270-767-56	Sequence 56, Appl
C 45	141	7.5	438	4	US-09-270-767-15338	Sequence 15338, A

#### ALIGNMENTS

##### RESULT 1

US-09-236-080-5  
; Sequence 5, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236, 080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1994  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-236-080-5

Alignment Scores:  
Pred. No.: 9.67e-237 Length: 1994  
Score: 1870.00 Matches: 368  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.31% Indels: 0  
DB: 3 Gaps: 0

US-09-655-272-4 (1-370) x US-09-236-080-5 (1-1994)

QY	1	MetAlaLaProAspLeuLeuAspProLysSerAlaGlnAsnSerLysProArgLeu	20
DB	484	ATGGCGGCCCTGACTTGTGGATCCAAAGTCTGTGCTCAGAACTCCAAACCGAGGCTC	543
QY	21	SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
DB	544	TCATTCCTCTTCAAAACCCACCGGTGCTTGTCTCCCGGGTGAGAGTACTCGGCATTAT	603



Qy 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
Db 729 GCCATTTATTTGTGGTTATCACTAAACAACTATTGGATTGGTGAAGTTCAGGT 788  
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
Db 789 GGATCCGATATTGAATATCTGGACTCTTATAGCCTGTCTGGTGTCTGGATCCCTGTGA 848  
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
Db 849 GGGCTGCTTACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908  
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpTrpAlaAsn 320  
Db 909 AAAAAGACAAAGAGAGGTGGAGAGTTCAGAGCACACGCTGCTGAGTGACAGCCAAC 968  
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
Db 969 GTACAGCCGGAATTCAGAAACACGAGGAGGAGTGTGAGTGTGAGATTTATGACAGTTC 1028  
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
Db 1029 CAGCGGCCACCTCCATCAAGCGGAGCTCTCGGCAGAACTGGCTGGAAACCAATCAG 1088  
Qy 361 GluLeuThrProCysMetArgThr 368  
Db 1089 GAGCTGACTCTTGTAGGAGACC 1112

## RESULT 3

US-09-336-643A-82  
; Sequence 82, Application US/09336643A  
; Patent No. 6399761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/09/336,643A  
; CURRENT FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82  
; LENGTH: 3300  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (50) ... (1285)  
US-09-336-643A-82

Alignment Scores:  
Pred. No.: 1,76e-231 Length: 3300  
Score: 1833.00 Matches: 356  
Percent Similarity: 98.91% Conservative: 8  
Best Local Similarity: 96.74% Mismatches: 4  
Query Match: 97.34% Indels: 0  
DB: 3 Gaps: 0

US-09-655-272-4 (1-370) x US-09-336-643A-82 (1-3300)

Qy 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
Db 50 ATGGGGCACCTGACTTGTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGCTC 109

Qy 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
Db 110 TCGTTTTCACGAAACCCACAGTGTCTCCCGGTGGAGAGTGCACAGCAATTAAT 169  
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrLeuIle 60  
Db 170 GTTATGAATATGAAGACGGTCTCCAGATATCTCGGTGGTGTCTCTATCTGATCATC 229  
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80  
Db 230 GGAGCCACCGTGTTCAAAGCAATTTGGAGAGCCTCATGAGATTTTCACAGAGACCACCAT 289  
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
Db 290 GTGATCCAGAAGCAAAATTCATATCCCAACATTCCTGTGTCAATTCGACGAGCTGGAT 349  
Qy 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
Db 350 GAATCATTCAGCAATATAGTGGCAGCAATTAATGCAGGGATTAATACGTTAGGAACACC 409  
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
Db 410 TCCAATCAATCAGTCAGTGGGATTTGGGAAGTTCCTCTCTTTCTGGCACTGTTATT 469  
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160  
Db 470 ACAACCATAGGATTTGGAACATCTCACCACGCACAGAAAGCGCGCAAAATATTCTGTATC 529  
Qy 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsnGln 180  
Db 530 ATCTATGCTCTTACTGGGAATTCCTCTCTTTGGTTTCTCTTGGCTGGAGTGGAGATCAG 589  
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
Db 590 CTAGGCACCATATTTGGAAGAAATTCGCAAGTGGAGATACGTTTATTAAGTGAAT 649  
Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
Db 650 GTTAGTCAGACCAAGATTCGCATCATCTCAACAATCATATTTATCTATTGGCTGTGTA 709  
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
Db 710 CTCTTTGTGGCTCTGCTCGCATCATATTCAAAACACATAGAGCTGGAGTGCCTGGAC 769  
Qy 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
Db 770 GCCATTTATTTGTGGTTATCACTCTAACAACTATTGGATTGGTGTGCTGAGTGCAGGT 829  
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
Db 830 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGTCTGTGTGTCTGGATCCTTGTGA 889  
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
Db 890 GGGCTTGTCTTACTTTCTGCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 949  
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpTrpAlaAsn 320  
Db 950 AAAAGACAAAGAGAGGTGGAGAGTTCAGAGCACACGCTGCTGAGTGCACAGCAAC 1009  
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
Db 1010 GTCACAGCGAAATTCAAAGAAACCCAGAGGCGAGTGTGAGATTTATGACAAAGTTC 1069  
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
Db 1070 CAGCGGGCCACCTCCATCAAGCGGAGGAGTCTCGGCAGAACTGGCTGGAAACCAATCAG 1129  
Qy 361 GluLeuThrProCysMetArgThr 368  
Db 1130 GAGCTGACTCTTGTAGGAGGACC 1153

RESULT 4



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; LENGTH: 1182
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-432-470-1

Alignment Scores:
Pred. No.: 3,69e-95 Length: 1182
Score: 797.00 Matches: 145
Percent Similarity: 72.18% Conservative: 60
Best Local Similarity: 51.06% Mismatches: 77
Query Match: 42.33% Indels: 2
DB: Gaps: 1

US-09-655-272-4 (1-370) x US-09-432-470-1 (1-1182)
QY 42 MetLysTrpLysThrValSerThrIlePheLeuValValLeuThrIleValGly 61
DB 1 ATGCGCAGCAGCAGCTCTCGGCCCTGCTGGCGCTGTCTTACTTGTGTCTGT 60
QY 62 AlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIleVal 81
DB 61 GCCTGTGTTCGGGCTCTGGAGCAGCCACAGCAGCAGCAGCAGCAGCAGCAGC 120
QY 82 IleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAspGlu 101
DB 121 GAGTCCGAGAGAGAGTTCCTGAGGCCCATCTCGTGTGAGCAGCAGCAGCAGC 180
QY 102 LeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSerSer 121
DB 181 CTCATCAAGAGAGTGTGCTGATGCCCTGGGAGGGGGTGGCAGCCAGAACCACTGACC 240
QY 122 AsnGlnValSerHis-----TrpAspLeuGlySerSerPhePheAlaGlyThrVal 139
DB 241 AGCAACAGCAGCAGCAGCTCAGCCTGGGACCTGGGAGCGGCTCTTTTCTCAGGAGCATC 300
QY 140 IleThrThrIleGlyPheGlyAsnIleSerProArgThrCluGlyLysIlePheCys 159
DB 301 ATCACCACCATCGCTATGCAATGTGGCCATGTGGCCATGTGGCCATGTGGCCATGT 360
QY 160 IleIleValAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsp 179
DB 361 ATCTTTATGCGTGTGGGATTCCTGCTGTGGGATCTCTATCGGAGGGGTGGGGAC 420
QY 180 GlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrp 199
DB 421 CGGCTGGGCTCTCTCCCTCGCCCATGCGATCGGTACATTCAGAGCCATCTTCTTGAAGTGG 480
QY 200 AsnValSerGlnThrLysIleArgIleIleSerThrIleIlePheIlePheGlyCys 219
DB 481 CAGTGTCCACCGGAGGTAGTAGAGTGTGTGTGGGATGCTTTTCTGCTGATCGGCTGC 540
QY 220 ValLeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeu 239
DB 541 CTGCTCTTTGCTCTCAGCCAGCAGTTCGTGTCTGTATATGAGGAGCAGGAGCAGTGG 600
QY 240 AspAlaIleTrpPheValValIleThrLeuThrIleGlyPheGlyAspThrValAla 259
DB 601 GAGGCCATCTACTTGTTCATAGTAGCGCTTACCACCGTGGGCTTGGGAGCTATGTGGCC 660
QY 260 GlyCysSerAspIleGluTrpLeuAspPheThrLysProValValTrpPheTrpIleLeu 279
DB 661 GCGCGCGAGACCCAGGAGGAGTCCCGGCCCTATCAGCCGCTGTGTGTGTGTGTGTGTGT 720
QY 280 ValGlyLeuAlaTrpPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIle 299
DB 721 CTGCGCTGTGCTTACTTCTGCTCAGTGTCTCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
QY 300 SerLysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAla 319
DB 781 TCCGCGCAGCAGTCCGCGAGAGATGGGCGGCTCAGCGCTCAGCGCTCAGCGCTCAGCG 840
QY 320 AsnValThrAla 323
DB 320 AsnValThrAla 323
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DB 841 ACAGTGACAGCG 852

RESULT 6
US-09-432-470-3
; Sequence 3, Application US/09432470
; Patent No. 6436197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; CURRENT FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-432-470-3

Alignment Scores:
Pred. No.: 3,88e-95 Length: 1218
Score: 797.00 Matches: 145
Percent Similarity: 72.18% Conservative: 60
Best Local Similarity: 51.06% Mismatches: 77
Query Match: 42.33% Indels: 2
DB: Gaps: 1

US-09-655-272-4 (1-370) x US-09-432-470-3 (1-1218)
QY 42 MetLysTrpLysThrValSerThrIlePheLeuValValLeuThrIleValGly 61
DB 37 ATGCGCAGCAGCAGCAGCTCTCGGCCCTGCTGGCGCTGTCTTACTTGTGTCTGT 96
QY 62 AlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIleVal 81
DB 97 GCCTGTGTTCGGGCTCTGGAGCAGCCACAGCAGCAGCAGCAGCAGCAGCAGC 156
QY 82 IleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAspGlu 101
DB 157 GAGTCCGAGAGAGTTCCTGAGGGGCCATCTCGTGTGTGAGCAGCAGCAGCAGC 216
QY 102 LeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSerSer 121
DB 217 CTCATCAAGAGAGTGTGCTATGCCCTGGGAGGGGGTGGGAGCCAGAACCACTGACC 276
QY 122 AsnGlnValSerHis-----TrpAspLeuGlySerSerPhePheAlaGlyThrVal 139
DB 277 AGCAACAGCAGCAGCAGCTCAGCCTGGGACCTGGGAGCGGCTCTTTTCTCAGGAGCATC 336
QY 140 IleThrThrIleGlyPheGlyAsnIleSerProArgThrCluGlyLysIlePheCys 159
DB 337 ATCACCACCATCGCTATGCAATGTGGCCCTCGCAGCAGATGCCGGGCGCTCTTCTGC 396
QY 160 IleIleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsp 179
DB 397 ATCTTTATGCGTGTGTGGGATTCCTGCTGTGTGGGATCTCTTCTGAGGAGCGGAGC 456
QY 180 GlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrp 199
DB 457 CGGCTGGGCTCTCTCCCTGGCCATGTCATCGGTACATTCAGAGCCATCTTCTTGAAGTGG 516
QY 200 AsnValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCys 219
DB 517 CAGCTGCCACCGAGAGTAGTAGAGTGTGTGCGGATGCTTTTCTGCTGATCGGCTGC 576
QY 220 ValLeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeu 239
DB 220 ValLeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeu 239
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SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 321

TYPE: DNA

ORGANISM: Homo sapiens

US-09-236-080-3

Alignment Scores:

Pred. No.: 4,98e-63 Length: 321  
Score: 547.00 Matches: 105  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.13% Mismatches: 0  
Query Match: 29.05% Indels: 0  
DB: 3 Gaps: 0

US-09-655-272-4 (1-370) x US-09-236-080-3 (1-321)

```
QY 119 AsnSerSerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThr 138
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 AACACCTCCCAATCAATCAGTCACTGGGATTTGGGAAGTTCTTCTTTTGTGGCACT 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 139 ValIleThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePhe 158
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GTTATTACACCATAGGATTTGGAAACATCTCACCGACACAGAGGGCGCAAAATATTC 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 159 CysIleIleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGly 178
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TGTATCATCATGCTTACTTGGGAATTCCTCTTGGTTTCTTCTTGGCTGGAGTTGGA 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 AspGlnLeuGlyThrIlePheGlyGlyGlyIleAlaLysValGluAspThrPheIleLys 198
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 GATCAGCTAGGCACCATATTATTGAAAGAGGAATTCGCAAGTGGAAATACGTTTATTAAG 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 199 TrpAsnValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGly 218
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TGGAAATGTAGTCAGACCAAGATTCGCATCATCTCACATCATATTTATCTATTGGC 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 219 CysValLeuPheValAlaLeu 225
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 TGTGTACTCTTTGTGGCTCTG 321
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 9

US-09-561-763-3

Sequence 3, Application US/09561763

Patent No. 6664373

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A. J. et al.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: MNI-074CP2

CURRENT APPLICATION NUMBER: US/09/561,763

CURRENT FILING DATE: 2000-04-29

PRIOR APPLICATION NUMBER: 09/431,367

PRIOR FILING DATE: 01-11-1999

PRIOR APPLICATION NUMBER: US 09/259,951

PRIOR FILING DATE: 01-03-1999

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 1497

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1497)

US-09-561-763-3

Alignment Scores:

Pred. No.: 1.2e-44 Length: 1497  
Score: 416.50 Matches: 97  
Percent Similarity: 51.10% Conservative: 66  
Best Local Similarity: 30.41% Mismatches: 131  
Query Match: 22.12% Indels: 26  
DB: 4 Gaps: 8

US-09-655-272-4 (1-370) x US-09-561-763-3 (1-1497)

```
QY 54 ValValLeuTyzIleuIleIleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnGlu 73
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 34 ATCATCTTCTACTTGGCCATCGGGCGGCGATCTTCTGAAGTGTCTGGAGGAGCCACACTGG 93
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 74 IleSerGlnArgThrThrIleValIleGlnLysGlnThrPheIleAlaGlnHisAlaCys 93
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 94 AAGGGAGGCCAAGAAAACCTACTACACACAGAAGTGCATCTGCTCAAGGATTTCCCGTGC 153
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 94 ValAsnSerThrGluLeuAspGluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGly 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 154 CTGGGTCAAGGAGGCGCTGGACAAGATCTTAGAGTGTGTATCTGATCTCTGACGACAGGGT 213
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 114 IleLeuProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGlySerSerPhe 133
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 214 GTGGCCATCATCAGGGAACCCAGACC-----TTCAACAACCTGGAACTGGCCCAATGCAATG 267
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 134 PhePheAlaGlyThrValIleThrIleGlyPheGlyAsnIleSerProArgThrGlu 153
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 268 ATTTTTCGACGACCGCTCATTTACCACTTGGATATGCAATGTGCTCCCAAGACCCCC 327
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 154 GlyGlyLysIlePheCysIleIleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeu 173
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 328 GCGGTGCGCTCTTCTGTGTCTTCTATGCTCTTCTCGGGGTGCGGCTC-----TGC 378
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 174 LeuAlaGlyValClyAspGlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGlu 193
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 379 CTGACGTGATC---AGTCCCTTGGGCAAGTCTTCTGGGGGAGCGTCCCAAGAGACTAGGG 435
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 194 AspThrPheIleLysTrpAsnValSerGlnThrLysIleArgIleIleSerThrIleIle 213
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 436 CAGTTCTTTACCAAGAGAGGTGTGAGTCTGCGAAGGCGCAGATCATCGTGCACAGTCATC 495
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 214 PheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePheLysHisIle 233
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 496 TTCATCGTGTGGGGCGTCTTAGTCCACCTGGTGATCCCACTTCTGATTTCTATGTTGACT 555
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 234 GluGlyTrpSerAlaLeuAspAlaIleTrpValValIleThrLeuThrThrIleGly 253
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 556 GAGGGGTGGAACCTACATCGAGGGCTCTACTACTCTTCTCATCACCATCTCCACCATCGGC 615
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 254 PheGlyAspTrpValAlaGly---GlySerAspIleGluTrpLeuAspPheTrpLysPro 272
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 616 TTCGTGACTTTTGTGGCGGTGTGAACCCAGCCCACTACCCAGCCCTGTACCGCTAC 675
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 273 ValValTrpPheTrpIleLeuValGlyLeuAlaTrpPheAlaAlaValLeuSerMetIle 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 676 TTCGTGAGCTCTGGATCTACTTGGGGCTGGCTGG-----CTGTCCCTTTT 723
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 293 GlyAspTrpLeu-----ArgValIleSerLysLysThrLys 304
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 724 GTCACTGGAAGTGAGCATGTTTGTGGAAGTCCACAAAGCCATTGAAGCGCGCGCGG 783
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 305 GluGluValGlyGluPheArgAla-----HisAlaAlaGluTrpThrAlaAsnValThr 322
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 784 CGACGGAAGGAGTCTTTGAGAGCTCCCCACACTCCCG--GAAGGCCCTGCAGGTGAAGGG 842
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 323 AlaGluPheLysGluThrArgArgLeuSerValGluIleTrpAspLysPheGlnArg 342
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 843 GAGCAGACGCTCCCAAGGAGCTCAACATCTTACGCTT-----TCTTTTCCAGAA 890
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 343 AlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGlu 361
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 891 GGAAGAGACCTACACGACCTCATCAGCAGATCGGGAAGAGGCCCATGAAGCAAG 947
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 10

US-09-431-367B-3

Sequence 3, Application US/09431367B

Patent No. 6670149

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A. J.



;; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

;; FILE REFERENCE: MNI-074CP

;; CURRENT APPLICATION NUMBER: US/09/431,367B

;; CURRENT FILING DATE: 1999-11-01

;; PRIOR APPLICATION NUMBER: 09/259,951

;; PRIOR FILING DATE: 1999-03-01

;; NUMBER OF SEQ ID NOS: 12

;; SOFTWARE: Patent In Ver. 2.0

;; SEQ ID NO 3

;; LENGTH: 1497

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (1)...(1497)

US-09-431-367B-3

Alignment Scores:

Pred. No.: 1,2e-44 Length: 1497

Score: 416.50 Matches: 97

Percent Similarity: 51.10% Conservative: 66

Best Local Similarity: 30.41% Mismatches: 131

Query Match: 22.12% Indels: 26

DB: 4 Gaps: 8

US-09-655-272-4 (1-370) x US-09-431-367B-3 (1-1497)

Qy 54 ValValLeuTyrLeuLeuIleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnGlu 73

Db 34 ATCATCTTCTACCTGGCCATCGGGGGCGGATCTTGAAGTGTGGAGGAGCCACACTGG 93

Qy 74 IleSerGlnArgThrIleValIleGlnLysGlnThrPheIleAlaGlnHisAlaCys 93

Db 94 AAGGAGCCAGAAAATACTACTACACAGAGTGCATCTGCTCAAGAGTTCCTCGTGC 153

Qy 94 ValAsnSerThrGluLeuAspGluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGly 113

Db 154 CTGGGTGAGGAGGCGCTGGACAGATCTAGAGGTGTATCTGATCTGACGAGGAGGTT 213

Qy 114 IleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGlySerPhe 133

Db 214 GTGGCCATCAGAGGAACAGACC-----TTCAACAACTGGAACTGGCCCAATGCAATG 267

Qy 134 PhePheAlaGlyThrValIleThrIleGlyPheGlyAsnIleSerProArgThrGlu 153

Db 268 ATTTTTCAGGAGCGCTATTACCACTTGGATGCAATGGTGGTCCCAAGACCCCC 327

Qy 154 GlyGlyLysIlePheCysIleIleTyrAlaLeuGluGlyIleProLeuPheGlyPheLeu 173

Db 328 GCGGTGCGCTCTTCTGTGTCTTATGTTCTTCTTGGGGTGGCGCTC-----TGC 378

Qy 174 LeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGlu 193

Db 379 CTGACGTGATC---AGTGCCTGGGCAAGTTCTCGGGGACGCTGCAAGAGACTAGG 435

Qy 194 AspThrPheIleLysTrpAsnValSerGlnThrLysIleArgIleIleSerThrIleIle 213

Db 436 CAGTCTCTTACCAGAGAGGTTGAGTCTGCGGAGGCGGAGATCAGCTGACAGTCACTC 495

Qy 214 PheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePheLysHisIle 233

Db 496 TTATCGTGTGGGGCTCTAGTCACCTGTGATCCACACCTTCGTATTATCATCGTCACT 555

Qy 234 GlnGlyTrpSerAlaLeuAspAlaIleTyrPheValIleThrLeuThrIleGly 253

Db 556 GAGGGGTGGATACATCAGGGGCTCTACTCTTCTTCACTCACTCACTCACTCACTCGG 615

Qy 254 PheGlyAspTyrValAlaGly---GlySerAspIleGluTyrLeuAspPheTyrLysPro 272

Db 616 TTCGTGACTTGTGGCGGTTGTGAACCCAGCGCAACTACCAAGCCCTGTACCGGTAC 675

Qy 273 ValValTrpPheThrIleLeuValGlyLeuAlaTyrPheAlaAlaValLeuSerMetIle 292

Db 277 ATTTTTCAGGAGCGCTGATTCATTCACCACTTGGATATGGCAATGTGCTCCCAAGACCCC 336

Db 676 TTCGFGAGCTCTGATCTACTTGGGGTGGCTGG-----CTGTCCTCTTTT 723

Qy 293 GlyAspTrpLeu-----ArgValIleSerLysLysThrLys 304

Db 724 GTCACTGGAAGGTGAGCATGTTTGTGAAGTCCACAAGCAATTAAAGCGGCGGG 783

Qy 305 GluGluValGlyGluPheArgAla-----HisAlaAlaGluTrpThrAlaAsnValThr 322

Db 784 CGACGGAAGGAGTCTCTTTGAGAGTCCCCACACTCCCG-GAAGGCCCTGCGAGGTGAAGG 842

Qy 323 AlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPheGlnArg 342

Db 843 GAGCAGACCTCCAAAGGAGCTCAACATCTTCAGCTT-----TCTTTCACAA 890

Qy 343 AlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGlu 361

Db 891 GGAAGAGACCTACACGACCTCATCAAGCAGATCGGGAAGAGGCGCATGAAGACAAG 947

RESULT 11

US-09-561-763-1

;; Sequence 1, Application US/09561763

;; Patent No. 6664373

;; GENERAL INFORMATION:

;; APPLICANT: Curtis, Rory A. J. et al.

;; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

;; FILE REFERENCE: MNI-074CP2

;; CURRENT APPLICATION NUMBER: US/09/561,763

;; CURRENT FILING DATE: 2000-04-29

;; PRIOR APPLICATION NUMBER: 09/431,367

;; PRIOR FILING DATE: 01-11-1999

;; PRIOR APPLICATION NUMBER: US 09/259,951

;; PRIOR FILING DATE: 01-03-1999

;; NUMBER OF SEQ ID NOS: 12

;; SOFTWARE: Patent In Ver. 2.0

;; SEQ ID NO 1

;; LENGTH: 3452

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (10)...(1506)

US-09-561-763-1

Alignment Scores:

Pred. No.: 4,84e-44 Length: 3452

Score: 416.50 Matches: 97

Percent Similarity: 51.10% Conservative: 66

Best Local Similarity: 30.41% Mismatches: 131

Query Match: 22.12% Indels: 26

DB: 4 Gaps: 8

US-09-655-272-4 (1-370) x US-09-561-763-1 (1-3452)

Qy 54 ValValLeuTyrLeuLeuIleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnGlu 73

Db 43 ATCATCTTCTACCTGGCCATCGGGGGCGGATCTTGAAGTGTGGAGGAGCCACACTGG 102

Qy 74 IleSerGlnArgThrIleValIleGlnLysGlnThrPheIleAlaGlnHisAlaCys 93

Db 103 AAGGAGCCAGAAAATACTACTACACAGAGTGCATCTGCTCAAGAGTTCCTCGTGC 162

Qy 94 ValAsnSerThrGluLeuAspGluLeuIleGlnIleValAlaAlaIleAsnAlaGly 113

Db 163 CTGGGTGAGGAGGCGCTGGACAGATCTCTAGAGGTGTATCTGATCTGACGAGGAGGT 222

Qy 114 IleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGlySerPhe 133

Db 223 GTGGCCATCAGAGGAGCCAGACC-----TTCAACAACTGGAACTGGCCCAATGCAATG 276

Qy 134 PhePheAlaGlyThrValIleThrIleGlyPheGlyAsnIleSerProArgThrGlu 153

Db 277 ATTTTTCAGGAGCGCTGATTCATTCACCACTTGGATATGGCAATGTGCTCCCAAGACCCC 336

QY 154 GlyGlyLysLeuPheCysIleIleThrAlaLeuLeuGlyIleProLeuPheGlyPheLeu 173  
DB 337 GCCGGTCGCTCTCTGTCTTCTATGCTCTTCCGGGGTGGCGCTC-----TGC 387  
QY 174 LeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGlu 193  
DB 388 CTGACGTGGATC---AGTGCCTTGGGCAAGTCTTTCGGGGGAGCTGCCAAGACTAGG 444  
QY 194 AspThrPheIleLysTrpAsnValSerGlnThrLysIleArgIleIleSerThrIle 213  
DB 445 CAGTTCCTTACCAAGAGAGGTGTGAGTCTCGGCAAGCGGCAGATCAGTGCACAGTCATC 504  
QY 214 PheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePheLysHisIle 233  
DB 505 TTCTATCGTGTGGGGCGCTCTAGTCCACCTCGTGTATCCACCTTCCTATTCATGGTGACT 564  
QY 234 GluGlyTrpSerAlaLeuAspAlaIleThrPheValIleThrLeuThrIleGly 253  
DB 565 GAGGGGTGGAACTACATCGAGGGCTTACTACTCTTCTATCACCATCTCCACCATCGGC 624  
QY 254 PheGlyAspTyrValAlaGly---GlySerAspIleGluTyrLeuAspPheTyrLysPro 272  
DB 625 TTCGGTGACTTGTGGCGGTGTGAACCCAGCGCCAACTACCACGCCCTGTACCGCTAC 684  
QY 273 ValValTrpPheTrpIleLeuValGlyLeuAlaTyrPheAlaValIleLeuSerMetIle 292  
DB 685 TTCGTGAGCTCTGGATCTACTTGGGGCTGGCTGG-----CTGTCCCTTTT 732  
QY 293 GlyAspTrpLeu-----ArgValIleSerLysLysThrLys 304  
DB 733 GTCACTGGAAAGTGAGTATGTTTGGGAAGTCCACAAAGCCATTAAAGAGCGCGCGG 792  
QY 305 GluGluValGlyGluPheArgAla-----HisAlaAlaGluTrpThrAlaAsnValThr 322  
DB 793 CGACGGAAAGAGTCTTTGAGAGCTCCCACTCCCG-CAAGGCCCTGCGAGTGAAGG 851  
QY 323 AlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPheGlnArg 342  
DB 852 GAGCAGACGCTCCAAAGAGCTCAACATCTTCAGCTT-----TCTTTCCAAGAA 899  
QY 343 AlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGlu 361  
DB 900 GGAAGAGACCTACACGACCTCATCAGCAGATCGGGAGAGGCCATGAGACAAG 956

## RESULT 12

US-09-431-367B-1  
; Sequence 1, Application US/09431367B  
; Patent No. 6670149  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP  
; CURRENT APPLICATION NUMBER: US/09/431,367B  
; CURRENT FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 09/259,951  
; PRIOR FILING DATE: 1999-03-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3452  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10)..(1506)  
US-09-431-367B-1

Alignment Scores:  
Pred. No.: 4,84e-44 Length: 3452  
Score: 416.50 Matches: 97  
Percent Similarity: 51.10% Conservative: 66  
Best Local Similarity: 30.41% Mismatches: 131  
Query Match: 22.12% Indels: 26

DB: 4 Gaps: 8  
US-09-655-272-4 (1-370) x US-09-431-367B-1 (1-3452)  
QY 54 ValValLeuTyrLeuIleIleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnGlu 73  
DB 43 ATCATCTTCTACTGCGCATCGGGCGGCGATCTTCGAAGTGTGGAGGAGCCACACTGG 102  
QY 74 IleSerGlnArgThrThrIleValIleGlnLysGlnThrPheIleAlaGlnHisAlaCys 93  
DB 103 AAGGAGGCCAAGAAAACTACTACACAGAAGCTCATCTGCTCAAGGAGTTCCTCGTGC 162  
QY 94 ValAsnSerThrGluLeuAspGluLeuIleGlnIleValAlaAlaIleAsnAlaGly 113  
DB 163 CTGGGTGAGGAGCGCTCGACCAAGATCTAGAGGTGTATCTGATCTCGAGGACAGGGT 222  
QY 114 IleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGlySerSerPhe 133  
DB 223 GTGGCCATCACAGGAGNACCAGACC-----TTCAACAACCTGGAACTGGCCCAATG 276  
QY 134 PhePheAlaGlyThrValIleThrIleGlyPheGlyAsnIleSerProArgThrGlu 153  
DB 277 ATTTTTCAGCGACCGCTCATACCACTTGATATGGCAATGTGGCTCCCAAGACCCCC 336  
QY 154 GlyGlyLysIlePheCysIleIleThrAlaLeuLeuGlyIleProLeuPheGlyPheLeu 173  
DB 337 GCCGGTCGCTCTCTGTCTTCTATGCTCTTTCGGGGTGGCGCTC-----TGC 387  
QY 174 LeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGlu 193  
DB 388 CTGACGTGATC---AGTCCCTTGGCAAGTCTTTCGGGGGAGCTGCCAAGAGACTAGG 444  
QY 194 AspThrPheIleLysTrpAsnValSerGlnThrLysIleArgIleIleSerThrIle 213  
DB 445 CAGTTCCTTACCAAGAGAGGTGTGAGTCTCGGCAAGCGGCAGATCAGTGCACAGTCATC 504  
QY 214 PheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePheLysHisIle 233  
DB 505 TTCTATCGTGTGGGGCTCTCTAGTCCACCTGGTGATCCCACTTCCTATTCATGCTGACT 564  
QY 234 GluGlyTrpSerAlaLeuAspAlaIleThrPheValIleThrLeuThrIleGly 253  
DB 565 GAGGGGTGGAACTACATCGAGGGCTTACTACTCTTCTATCACCATCTCCACCATCGGC 624  
QY 254 PheGlyAspTyrValAlaGly---GlySerAspIleGluTyrLeuAspPheTyrLysPro 272  
DB 625 TTCGGTGACTTGTGGCGGTGTGAACCCAGCGCCAACTACCACGCCCTGTACCGCTAC 684  
QY 273 ValValTrpPheTrpIleLeuValGlyLeuAlaTyrPheAlaValIleLeuSerMetIle 292  
DB 685 TTCGTGAGCTCTGGATCTACTTGGGGCTGGCTGG-----CTGTCCCTTTT 732  
QY 293 GlyAspTrpLeu-----ArgValIleSerLysLysThrLys 304  
DB 733 GTCACTGGAAAGTGAGTATGTTTGGGAAGTCCACAAAGCCATTAAAGAGCGCGCGG 792  
QY 305 GluGluValGlyGluPheArgAla-----HisAlaAlaGluTrpThrAlaAsnValThr 322  
DB 793 CGACGGAAAGAGTCTTTGAGAGCTCCCACTCCCG-CAAGGCCCTGCGAGTGAAGG 851  
QY 323 AlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPheGlnArg 342  
DB 852 GAGCAGACGCTCCAAAGAGCTCAACATCTTCAGCTT-----TCTTTCCAAGAA 899  
QY 343 AlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGlu 361  
DB 900 GGAAGAGACCTACACGACCTCATCAGCAGATCGGGAGAGGCCATGAGACAAG 956

RESULT 13  
US-09-162-842-13  
; Sequence 13, Application US/09362842  
; Patent No. 6511824  
; GENERAL INFORMATION:

```

; APPLICANT: Buchman et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK
; TITLE OF INVENTION: CHANNELS AND METHODS OF USE
; FILE REFERENCE: 7326-104
; CURRENT APPLICATION NUMBER: US/09/362,842
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Leptinotarsa decemlineata
; US-09-362-842-13

Alignment Scores:
Pred. No.: 2,296-42 Length: 1086
Score: 397.50 Matches: 102
Percent Similarity: 54.63% Conservative: 69
Best Local Similarity: 32.59% Mismatches: 107
Query Match: 21.11% Indels: 36
DB: Gaps: 8

US-09-655-272-4 (1-370) x US-09-362-842-13 (1-1086)
QY 24 SerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsnValMetLys 43
DB 56 ACAGAGAAATTCGGTTTACTTCCAAAATGTGGAAGGAATCGCAAAATTAITGGCA 115
QY 44 TplYsThrVal-----SerThrIlePheLeuValValValLeuYrLeuIle 59
DB 116 TGGAGAAACATTCCTTCGGTTTTCACGTATTATTATTGCTATTTC-ANGTTTTTGTCT 174
QY 60 IleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnIleuSerGlnAspThrThr 79
DB 175 AGCGGAGCAGCGGTTTTCAGTTTACGTCAGCACCTGAGGAACGGGCACGTAGAGATTAA 234
QY 80 IleValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeu 99
DB 235 CTTGGAAACAGCAGTACAAAATTTTGGTGTCTTAATCCTTAACGTACAGATCGAGATTG 294
QY 100 AspGluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsn 119
DB 295 GAAGAATTGATAGTAAATAGTACAGCAAAATTAATCGTGGAGTTTCAGCTATCGAAAT 354
QY 120 SerSerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrVal 139
DB 355 GCACATCTCAGAG--CCTAATTGGAGTTTGGTCAATCTTTCTTGGCACACAGTC 411
QY 140 IleThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCys 159
DB 412 ATCACAACATATAGGATATGTCATGTACTCCACTCAGCAGAAATGTTAAATTAITTCG 471
QY 160 IleIleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsp 179
DB 472 ATGTTTTATGCCGTGGTTTGGAAATTCCTTGACTCTGGTACTGCTTCTGCTCGTGGAA 531
QY 180 GlnLeu-----GlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIle 197
DB 532 CGAATTACTGATTCGAGATTTGG-----CTCTTG 561
QY 198 LysTrpAsnValSerGln-----ThrLysIleArgIleIleSer 210
DB 562 CAATGGCTTAATTCAAAATTAGGACACCTTTTATCAGCCTCTTCGAATACGAATCGTCCAT 621
QY 211 ThrIleIlePheIleLeuPheGlyCysValLeuPhePheAlaLeuProAlaValIlePhe 230
DB 622 TTGGCAATATATGTTTTAGTACTACTGTGTATTCTTCCTGCTACTCCACGATGCAATTTT 681
QY 231 LysHisIleGlu---GlyTrpSerAlaLeuAspAlaIleTyPheValIleThrLeu 249
DB 682 GCCTCTTTGAAACCAAGATGGCACTATTGGAATCTCTTACTACTTACTTCTTATATCCCTC 741

```

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Db 370 CCCAACGATGGTCCCGCTCTTCTGATCTTCTTTGCCCTTGGGGATCCCACTC 429
Qy 170 PheGlyLeuLeuAlaGlyValGlyAspGlnLeuGlyThrPheGlyLysGlyIle 189
Db 430 AACCTCTGGTGCTC-----AACCGACTGGGGCATCTCATGACGAGGAGTA 477
Qy 190 -----AlaLysValGluAspThrPheIleLysTrpAsnValSerGlnThrLys 205
Db 478 AACCACTGGGCGAGCGCTGGGGGCACC-----TGGCAG---GATCCTGACAAG 525
Qy 206 IleArgIleLeuSerThrIlePheIlePheGlyCysValLeuPheValAlaLeu 225
Db 526 GCGCGGTGGCTGGCGGCTCTGGCGCTCTCTCTGGGCTCTCTGCTTCTCTGGCTG 585
Qy 226 ProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAspAlaIleTyrPheVal 245
Db 586 CCACCGTGTCTTCTCCACATGAGGGCTGGAGCTACACAGAGGGCTTCTACTTCGCC 645
Qy 246 ValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGlyLysSerAspIleGlu 265
Db 646 TTCATCACCTCAGCACCGTGGGCTTCGGCGACTTACGTGATTGGAATGAACCCCTCCAG 705
Qy 266 ---TyrLeuAspPheTyrLysProValValTyrPheThrIleLeuValGlyLeuAlaTyr 284
Db 706 AGGTACCACTGTGGTACAAGACATGGTGTCTCTGGATCTCTTTTGGGATGGCATGG 765
Qy 285 PheAlaAlaValLeuSerMetIle 292
Db 766 CTGGCTTGATCATCAACTCATC 789
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## RESULT 15

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US-09-431-367B-6
; Sequence 6, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: WNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
US-09-431-367B-6
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Pred. No.: 4.86e-41 Length: 996
Score: 387.00 Matches: 88
Percent Similarity: 56.05% Conservative: 51
Best Local Similarity: 35.48% Mismatches: 95
Query Match: 20.55% Indels: 14
DB: 4 Gaps: 6
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US-09-655-272-4 (1-370) x US-09-431-367B-6 (1-996)

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Qy 70 GlnProGlnGluIleSerGlnArgThrIleValIleGlnLysGlnThrPheIleAla 89
Db 133 GGCGCGCGCGGCGGAGCTCCAGCGCAGCTTCCAGCGCGACAGTGGGAGCTGTTCAG 192
Qy 90 GlnHisAlaCysValAsnSerThrGluLeuAspGluLeuIleGlnIleValAlaAla 109
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Db 193 AACTTCACGTGTGAGCCGCCCGCTGGACTCCTGATCCGGGATGTCTGTCGAAGCA 252
Qy 110 IleAsnAlaGlyIleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeu 129
Db 253 TACAAAAACGGAGCCAGCTCTCTCAGACACACCAGCAGC---ATGGGGCGCTGGAGCTC 309
Qy 130 GlySerSerPhePhePheAlaGlyThrValIleThrThrIleGlyPheGlyAsnIleSer 149
Db 310 GTGGGCTCTCTCTCTTTCTGTGTCCACCATCACCACCATTTGGCTATGGCAACCTCAGC 369
Qy 150 ProArgThrGluGlyCysIlePheCysIleIleTyrAlaLeuLeuGlyIleProLeu 169
Db 370 CCCAACACATGGCTGCCGCTCTTCTGATCTCTTTGGCCTTGTGGGATCCCACTC 429
Qy 170 PheGlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIle 189
Db 430 AACCTCTGGTGCTC-----AACCGACTGGGGCATCTCATGACGAGGAGTA 477
Qy 190 -----AlaLysValGluAspThrPheIleLysTrpAsnValSerGlnThrLys 205
Db 478 AACCACTGGGCGAGCGCTGGGGGCACC-----TGGCAG---GATCCTGACAAG 525
Qy 206 IleArgIleLeuSerThrIlePheIleLeuPheGlyCysValLeuPheValAlaLeu 225
Db 526 GCGCGGTGGCTGGCGGCTCTGGCGCTCTCTCTGGGCTCTCTGCTTCTCTGCTGCTG 585
Qy 226 ProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAspAlaIleTyrPheVal 245
Db 586 CCACCGCTGCTTCTCTCCACATGAGGGCTGGAGCTACACAGAGGGCTTCTACTTCGCC 645
Qy 246 ValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGlyLysSerAspIleGlu 265
Db 646 TTCATCACCTCAGCACCGTGGGCTTCGGCGACTTACGTGATTGGAATGAACCCCTCCAG 705
Qy 266 ---TyrLeuAspPheTyrLysProValValTyrPheThrIleLeuValGlyLeuAlaTyr 284
Db 706 AGGTACCACTGTGGTACAAGACATGGTGTCTCTGGATCTCTTTTGGGATGGCATGG 765
Qy 285 PheAlaAlaValLeuSerMetIle 292
Db 766 CTGGCTTGATCATCAACTCATC 789
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Job time : 109.727 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 3, 2005, 01:34:36 ; Search time 648.464 Seconds  
(without alignments)  
3278.486 Million cell updates/sec

Title: US-09-655-272-4

Perfect score: 1883

Sequence: 1 MAAPDLDLPKSAQAKPRLL.....SABLGNHNOELTPCMTCL 370

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -OPMT=fastp -SUFFIX=rnpb -MINMATCH=0.1  
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Database :

Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1827	97.0	2391	18	US-10-349-528-9
5	1805	95.9	2130	8	US-08-816-011-46
6	1247.5	66.3	1614	11	US-09-892-360-1
7	1247.5	66.3	1632	10	US-09-852-386-34
8	1247.5	66.3	1644	15	US-10-332-175-1
9	1247.5	66.3	2028	16	US-10-262-511-105
10	1247.5	66.3	2065	9	US-09-729-920-1
11	1247.5	66.3	2065	18	US-10-887-932-1
12	1247.5	66.3	2730	16	US-10-302-172-432
13	1220	64.8	2820	16	US-10-332-447-42
14	797	42.3	1182	14	US-10-243-035-1
15	797	42.3	1257	9	US-09-828-035-1
16	797	42.3	1257	15	US-10-146-733-30
17	797	42.3	1260	15	US-10-345-680-45
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19	797	42.3	1408	9	US-09-828-035-1
20	797	42.3	1408	15	US-10-146-733-28
21	797	42.3	1408	15	US-10-352-684A-7
22	797	42.3	1408	15	US-10-391-399-18
23	797	42.3	2747	18	US-10-768-158-11
24	797	42.3	2772	15	US-10-345-680-43
25	797	42.3	3945	9	US-09-747-835A-30
26	797	42.3	3945	16	US-10-312-312-30
27	797	42.3	3996	9	US-09-747-835A-28
28	797	42.3	3996	15	US-10-037-270-195
29	797	42.3	3996	15	US-10-117-722-195
30	797	42.3	3996	16	US-10-312-312-28
31	645	34.3	401	9	US-09-867-701-5443
32	572.5	30.4	1265	16	US-10-276-774-1249
33	547	29.0	321	9	US-09-828-746-3
34	517	27.5	1009	18	US-10-343-903-38
35	506.5	26.9	2036	16	US-10-459-190-1
36	502.5	26.7	937	13	US-10-121-966-1
37	499.5	26.5	882	13	US-10-121-966-3
38	499.5	26.5	897	16	US-10-451-892-1
39	495.5	26.3	879	16	US-10-451-892-9
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41	495.5	26.3	2351	16	US-10-459-190-3
42	416.5	22.1	1497	9	US-09-735-169A-3
43	416.5	22.1	1497	9	US-09-735-171A-3
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ALIGNMENTS

RESULT 1  
US-09-828-746-5  
; Sequence 5, Application US/09828746  
; Patent No. US2002028485A1  
; GENERAL INFORMATION:  
; APPLICANT: Helen Jane Meadows  
; APPLICANT: Conrad Gerald Chapman  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30031-D1  
; CURRENT APPLICATION NUMBER: US/09/828,746  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: US 09/236,080  
; PRIOR FILING DATE: 1999-01-25  
; PRIOR APPLICATION NUMBER: EP 98300570.3  
; PRIOR FILING DATE: 1998-01-27  
; PRIOR APPLICATION NUMBER: UK 9822135.1  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1994

; TYPE: DNA			
; ORGANISM: HOMO SAPIENS			
US-09-828-746-5			
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Pred. No.:	1.02e-192	Length:	1994
Score:	1870.00	Matches:	368
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.31%	Indels:	0
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Qy	1	MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu	20
Db	484	ATGGCGCCCTGACTGCTGGATCCCAAGTCTGCTCAGAACTCCAAACCGAGGCTC	543
Qy	21	SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
Db	544	TCATCTCTTCAAAACCCACCGTCTTCCCGGTGGAGTGAATCGGCAATTAAT	603
Qy	41	ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuLysLeuIle	60
Db	604	GTATGAATGGAAGACAGCTCCACGATTTCTCGTGTGCTCTCTACCTGATCATC	663
Qy	61	GlyAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle	80
Db	664	GGAGCGCGGTGTTCAGAGCATGGAGCAGCTCCAGAGATTTCCCGAGGACCACT	723
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100
Db	724	GTGATCCAGAGCAGACCTTCATAGCCAGCATGCTCGCTCACTCCACGAGCTGGAC	783
Qy	101	GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120
Db	784	GAATCATCCAGCAATAGTGGCAGCAATTAACGAGGATTAATCCCTTAGGAAACAGC	843
Qy	121	SerIleGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle	140
Db	844	TCCAATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTTCTTGTGCTGCTGTTATC	903
Qy	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle	160
Db	904	ACAACCATAGGATTTGGAAACATCTCCCAAGCACTGAAGTGGAAATAATTTCTGCATC	963
Qy	161	IleValAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsnGln	180
Db	964	ATCTATGCTTGTGCGGAATTCCTCTTTGGCTTTCTACTGGCTGGGTGGTGTATCAG	1023
Qy	181	LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn	200
Db	1024	CTAGGAATATATTTGGAAAGGAATTCGAAGATGGGAAGACACATTTATTAGTGGAT	1083
Qy	201	ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal	220
Db	1084	GTATGTCAGACGACATTCGATCATCTCCACCATCATCTTCTCTTGTGCTGTGTC	1143
Qy	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp	240
Db	1144	CTCTTTGTGCTCTCCCTCGCGTCATATTCAGACATAGAGGCTGGAGCGCCCTGGAC	1203
Qy	241	AlaIleTrpPheValValIleThrLeuThrIleGlyPheGlyAspTrpValAlaGly	260
Db	1204	GCTATCTATTTGTGGTTATCACTCTGACGACCATTTGGATTGGAGACTAGTGGCAGGT	1263
Qy	261	GlySerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleLeuVal	280
Db	1264	GGATCAGACATTAATCTGACATCTACAGCCCTGTGGTGTGTTCTGATCCTCGTT	1323
Qy	281	GlyLeuAlaTrpPheAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer	300
Db	1324	GGGCTGGCCTACTTTTGCAGCTGTCTTGACATGATTTGGGACTGGCTGAGGTGATCTCT	1383

Qy	301	LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn	320
Db	1384	AGAAGACCAAGAGAGGTGGGAGATTTCAGACGGCATGCCGCTGAGTGGACAGCCAAT	1443
Qy	321	ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTrpAspLysPhe	340
Db	1444	GTACGGCCGAGTTCAAGGAACGAGGAGCGGCTGAGCGTGGAGATCTACGACAAGTTC	1503
Qy	341	GlnArgAlaThrSerValLysArgLysSerAlaGluLeuAlaGlyAsnHisAsnGln	360
Db	1504	CAGCGTGCACATCCGTGAAGCGGAAGCTCTCCGAGAGCTGGCGGCAACCAACCCAG	1563
Qy	361	GluLeuThrProCysMetArgThr	368
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RESULT 2

US-09-828-746-1

; Sequence 1, Application US/09828746

; Patent No. US20020028485A1

; GENERAL INFORMATION:

; APPLICANT: Helen Jane Meadows

; APPLICANT: Conrad Gerald Chapman

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP-30031-D1

; CURRENT APPLICATION NUMBER: US/09/828,746

; PRIOR FILING DATE: 2001-04-09

; PRIOR APPLICATION NUMBER: US 09/236,080

; PRIOR FILING DATE: 1999-01-25

; PRIOR APPLICATION NUMBER: EP 98300570.3

; PRIOR FILING DATE: 1998-01-27

; PRIOR APPLICATION NUMBER: UK 9822135.1

; PRIOR FILING DATE: 1998-10-09

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1246

; TYPE: DNA

; ORGANISM: HOMO SAPIENS

US-09-828-746-1

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

US-09-655-272-4 (1-370) x US-09-828-746-1 (1-1246)

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Qy	21	SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
Db	69	TCGTTTTTCCAGAAACCCACAGTGTCTTCCCGGTGGAGTGCACAGCATTAAAT	128
Qy	41	ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuTrpLysLeuIle	60
Db	129	GTATGAATGGAAGACGGTCTCCAGATATCTCTGTTGTTGCTCTCTATCTGATCATC	188
Qy	61	GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle	80
Db	189	GGAGCCACCGTGTTCAGAGCATTTGGAGCAGCTCATGAGATTTTCAGAGGACCACT	248
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100
Db	249	GTGATCCAGAAAGCAATTCATATCCCAACATCTCTGTGTCAATTCGACGAGCTGGAT	308
Qy	101	GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120



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Db 309 GAACTCATTGAGCAATAGTGGCAGCAATTAATGCAAGGATTATACCGTTAGAAACACC 368
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerPhePheAlaGlyThrValIle 140
Db 369 TCCAATCAATCAGTCAGTCAGTGGGATTTGGGAAGTTCCTCTCTTGTGCGCACTGTTATT 428
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysIle 160
Db 429 ACAACCATAGGATTTGGAACATCTCACACGCACAGAAAGCGGCAAAATATTTCTGTATC 488
Qy 161 IleTrpAlaLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180
Db 489 ATCTATGCTTACTGGGAATCCCTCTTGGTTTCTCTGCTGGAGTTGGAGATCAG 548
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 549 CTAGGCACCATATTTGGAAGAAGAAATGCAAGTGAAGATAGCTTTTAAAGTGAAT 608
Qy 201 ValSerGlnThrIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 609 GTTAGTCAGACCAAGATTCGCATCATCTCAACAATCATATTTATATCTATTTGGCTGTGTA 668
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
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Qy 241 AlaIleTrpPheValValIleThrLeuThrThrIleGlyPheGlyAspTrpValAlaGly 260
Db 729 GCCATTTATTTGTGGTTATCTCTCAACATATTGGATTGGTGACTACGTTGCAGT 788
Qy 261 GlySerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleLeuVal 280
Db 789 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGTCTGGTGGTTCTGGATCCTGTA 848
Qy 281 GlyLeuAlaTrpPheAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 849 GGGCTTGCTTACTTCTGCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 908
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Qy 361 GluLeuThrProCysMetArgThr 368
Db 1089 GAGCTGACTCTCTGTAGGAGACC 1112

RESULT 3
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; Sequence 82, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)....(1285)
US-10-121-746-82

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Score: 1833.00 Matches: 356
Percent Similarity: 98.91% Conservative: 8
Best Local Similarity: 96.74% Mismatches: 4
Query Match: 97.34% Indels: 0
DB: 14 Gaps: 0

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Db 50 ATGGCGGCACCTGACTTGTGGATCCTAAATCTGCGCTCAGAACTCCAAACCGAGGCTC 109
Qy 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 110 TCGTTTTCACAAACCCACAGTGTCTTCCGGGTGGAGTGACACGACCATTAAT 169
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuTrpIleLeuIle 60
Db 170 GTTATGAATGGAAGCGTCTCCAGATATTCCTGGTGTGTCTCTATCTGATCATC 229
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80
Db 230 CGAGGCACCGTGTTCAAAGCATTTGGAGCAGCCTCATGAGATTTTCACAGAGGACCCATT 289
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 290 GTGATCCAGAAACCAACATTCATATCCCAACATTCCTGTGCAATTCGACGGAGCTGGAT 349
Qy 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 350 GAATCATTCAGCAATAGTGGCAGCAATTAATGAGGATTTATACCGTTAGGAACACC 409
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 410 TCCAATCAATCAGTCAGTGGGATTTGGGAAGTTCCTCTCTTGTGCTGGCACTGTTATT 469
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysIle 160
Db 470 ACAACCATAGGATTTGGAACATCTCACACGCACAGAAAGCGGCAAAATATTTCTGTATC 529
Qy 161 IleTrpAlaLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180
Db 530 ATCTATGCTTACTGGGAATTCCTCTTGGTTTCTCTTGTGCTGGAGTTGGAGATCAG 589
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 590 CTAGGCACCATATTTGGAAGAAGAAATGCAAGTGAAGATACGCTTTTAAAGTGAAT 649
Qy 201 ValSerGlnThrIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 650 GTTAGTCAGACCAAGATTCGCATCATCTCAACAATCATATTTATATCTATTTGGCTGTGTA 709
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 710 CTCCTTTGTGGCTCTGCTCGCATCATATTCAACACATAGAGGCTGGAGTGCCTGGAC 769
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241 AlalleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
 770 GCCATTATTTTGTGGTATCACTCAACAACTATTGATTTGGTACTACGTTCAGGT 829  
 261 GlySerAspIleGluTyrLeuAspPheTyrIysProValValTrrPheTrrPheIleVal 280  
 830 GGATCCGATATTGAATATCTGGACTTCTATAGCCCTGTCTGGTCTGGATCCTTGT 889  
 281 GlyLeuAlaTyrPheAlaValIleLeuSerMetIleGlyAspTrrPheValIleSer 300  
 890 GGGCTTGGCTTACTTCT 949  
 301 LysLeuThrIysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrrPheAlaAsn 320  
 950 AAAAGACAAAGAGAGGTGGAGAGTTTCAGACACACCTGCTGAGTGGACGCCAAC 1009  
 321 ValThrAlaGluPheIysGluThrArgArgArgLeuSerValGluIleTyrAspIysPhe 340  
 1010 GTCACAGCCGAATTCAAAGAAACCCAGAGGCGACTGAGTGTGAGATTTATGACAAATTC 1069  
 341 GlnArgAlaThrSerValIysArgIysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 1070 CAGGGGCCACCTCCATCAAGCCGAGGCTCTGGCAGAACTGGCTGGAACCAACATCAG 1129  
 361 GluLeuThrProCysMetArgThr 368  
 1130 GAGCTGACTCTCTGTAGGAGGACC 1153  
 RESULT 4  
 US-10-349-528-9  
 ; Sequence 9, Application US/10349528  
 ; Publication No. US2004025368A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RAMANATHAN, Chandra  
 ; APPLICANT: GOPAL, Shuba  
 ; APPLICANT: MINIER, Gabe  
 ; APPLICANT: FEDER, John  
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF  
 ; FILE REFERENCE: D0210  
 ; CURRENT APPLICATION NUMBER: US/10/349,528  
 ; CURRENT FILING DATE: 2003-01-22  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO 9  
 ; LENGTH: 2391  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 US-10-349-528-9  
 Alignment Scores:  
 Pred. No.: 6,27e-188 Length: 2391  
 Score: 1827.00 Matches: 354  
 Percent Similarity: 98.91% Conservative: 10  
 Best Local Similarity: 96.20% Mismatches: 4  
 Query Match: 97.03% Indels: 0  
 DB: 18 Gaps: 0  
 US-09-655-272-4 (1-370) x US-10-349-528-9 (1-2391)  
 QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerIysProArgLeu 20  
 Db 586 TTGGCGGCACCTGACTTGTGGATCTCTAAATCTGCCGCTCAGAACTCCAAACCCGAGGCTC 645  
 QY 21 SerPheSerSerIysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 Db 646 TCGTATTTCCACGAACCCACAGTCTTCTCCCGGTGGAGTGCACGACCACTTAAT 705  
 QY 41 ValMetIysTrpIysThrValSerThrIlePheLeuValValValIleLeuIle 60  
 Db 706 GTTATGAATGAAGAGACGGCTCCACGATATCTCGTGGTGTCTCTCTATCTGATCATC 765  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnIleSerGlnArgThrThrIle 80

Db 766 GGAGCCACCGTGTTCARAGCATTTGAGCAGCTCATGAGATTTTCACAGAGACCACCAT 825  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 Db 826 GTGATCCAGAGCAACCAATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 885  
 QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 Db 886 GAACTCATTCAGCAATAAGTAGGCACCAATAAATGACGGGATATATACCTTAGGAAACACC 945  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 Db 946 TCCAAATCAAAATCAGTCTGGGATTTGGGAAGTTCCTCTCTCTCTCTCTCTCTCTCT 1005  
 QY 141 ThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyGlyGlyGlyPheCysIle 160  
 Db 1006 ACAACCATAGGATTTGGAAAGCAATCTCACCACGACAGAGGCGCAAAATATTTCTGTATC 1065  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 Db 1066 ATCTATGCTTACTGGGAATTTCCCTCTTTTGTCTCTCTCTCTCTCTCTCTCTCTCT 1125  
 QY 181 LeuGlyThrIlePheGlyGlyGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 Db 1126 CTAGGCACCATATTTGGAAAGCAATTTGCCAAGTGGAAAGATACGTTTATTAACTGGAAT 1185  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 Db 1186 GTTAGTCAGACCAAGATTCGCATCATCTCAACATCATATATATATATTTTGTCTGTGA 1245  
 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 Db 1246 CTCTTTGTGGCTCTGCTGCGATCATATCAACACATAGAGGCTGGAGTGCCTGGAC 1305  
 QY 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
 Db 1306 GCCATTATTTTGTGGTATCTCACTCAACATATTTGGTGGTACTACGTACGTGAGGT 1365  
 QY 261 GlySerAspIleGluTyrLeuAspPheTyrIysProValValTrrPheTrrPheIleVal 280  
 Db 1366 GGATCCGATATTGAATATCTGGACTTCTATAAGCTCTGTGTGTCTGTGTCTGTGT 1425  
 QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrrPheValIleSer 300  
 Db 1426 GGGCTTGTCTTACTTGTCTGCTCTGAGCATGATTTGAGATTTGGCTCCGAGTGTATCT 1485  
 QY 301 LysLeuThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrrPheAlaAsn 320  
 Db 1486 AAAAGACAAAGAGAGTGGAGAGTTCAAAGACACACGCTGCTGAGTGGACGCCAAC 1545  
 QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyrAspIysPhe 340  
 Db 1546 GTCACAGCCGAATTCAAAGAAACCCAGAGGCGACTGAGTGTGGAGATTTATGACAAATTC 1605  
 QY 341 GlnArgAlaThrSerValIysArgIysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 Db 1606 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGAGAACTGGCTGGAACCAACCAATCAG 1665  
 QY 361 GluLeuThrProCysMetArgThr 368  
 Db 1666 GAGCTGACTCTCTGTAGGAGGACC 1689  
 RESULT 5  
 US-08-816-011-46  
 ; Sequence 46, Application US/08816011  
 ; Publication No. US20030165806A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Price, Laura A.  
 ; APPLICANT: Pausch, Mark H.  
 ; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences  
 ; TITLE OF INVENTION: Encoding Them, and Methods of Using Same  
 ; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: American Home Products Corporation  
 ; STREET: One Campus Drive  
 ; CITY: Parsippany  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07054  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA: US/08/816,011  
 ; APPLICATION NUMBER: US/08/816,011  
 ; FILING DATE: 11-MAR-1997  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Matthews, Gale F.  
 ; REGISTRATION NUMBER: 32,269  
 ; REFERENCE/DOCKET NUMBER: 32,421-C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-683-2134  
 ; TELEFAX: 201-683-4117  
 ; INFORMATION FOR SEQ ID NO: 46:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2130 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-816-011-46

## Alignment Scores:

Pred. No.: 1.3e-185 Length: 2130  
 Score: 1805.00 Matches: 352  
 Percent Similarity: 98.37% Conservative: 10  
 Best Local Similarity: 95.65% Mismatches: 6  
 Query Match: 95.86% Indels: 0  
 DB: 8 Gaps: 0

US-09-655-272-4 (1-370) x US-08-816-011-46 (1-2130)

QY 1 MetAlaAlaProAspLeuLeuAppProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 DB 223 GTGGCGGACCTGACTTGTGGATCTCTAAATCTGCGCTCAGAACTCCAAACCGAGGCTC 282  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 DB 283 TCATTTTCACGAAACCCACAGTCTTGTCTCCGGGTGGAGTGCACGACCATTAAT 342  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIleIle 60  
 DB 343 GTTATGAATGGAAGACGGTCTCCAGATATCTCGTGTGTTCTCTATCTGATCATC 402  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
 DB 403 GGAGCACCGTGTTCAAAGCATTTGGAGCGCTCATGAGATTTTCACAGGAGCCACCAT 462  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 463 GTGATCAGAGAACCAATTCATATCCCAACATCTCTGTCTCAATTCGACGGAGCTGGAT 522  
 QY 101 GluLeuIleGlnGlnIleValAlaIleAsnAlaGlyIleIlePheProLeuGlyAsnSer 120  
 DB 523 GAACTCATTCAGCAATAGTGGCAGCAATAATGCGAGGATTATACCGTTAGGAACACC 582  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 DB 583 TCCAATCAATCAGTCACTGGGATTTGGGAAGTCTCTCTCTTCTGCTGCGACTGTATT 642  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 DB 643 ACAACCATAGGATTTGGAAACATCTCACCACGACAGAGGCGGAAAATATTTCTGTATC 702

QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 DB 703 ATCTATGCTTACTGGGAATTCCTCTTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG 762  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 DB 763 CTAGGCACCATATTTGGAAAAGGAATTGCAAGTGAAGATACGTTTATTAACTGGAAT 822  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIlePheIleLeuPheGlyCysVal 220  
 DB 823 GTTAGTCAGACCAAGATTCGCATCTCTCAACAATCATATTTATATACTATTGGCTGTGTA 882  
 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 883 CTCCTTTGTGGCTCTGCTCGCATCATATTCAAAACACATAGAAGCTGGAGTGCCTGGAC 942  
 QY 241 AlaIleTyrPheValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
 DB 943 GCAATTTATTTTGGTGTATCACTCTAACACATATTGGATTGGTGACTACGTTGAGGT 1002  
 QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
 DB 1003 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGCTGCTGTTCTGGATCTTGTGA 1062  
 QY 281 GlyLeuAlaTyrPheAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 1063 GGGCTTTGCTTACTTTGCTGCTGTCGTCGATGATTGGGAGATTGCTCGAGTGATATCT 1122  
 QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 DB 1123 AAAAGACAAAAGAGAGGTGGAGAGTTCAGAGCACGCTGCTGAGTGAGCAGCAAC 1182  
 QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
 DB 1183 GTCACAGCCGATTCAAAGAACACGAGGAGCTGAGTGTGGAGATTTATGACAGTTC 1242  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 DB 1243 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGCAAACTGCTGGAAACCAATCAG 1302  
 QY 361 GluLeuThrProCysMetArgThr 368  
 DB 1303 GAGTGACTCTCTTAGGAGGACC 1326

## RESULT 6

; US-09-892-360-1  
 ; Sequence 1, Application US/09892360  
 ; Publication No. US20040101833A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LAZDUNSKI, MICHEL  
 ; APPLICANT: LESAGE, FLORIAN  
 ; APPLICANT: ROMÉY, GEORGES  
 ; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE  
 ; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND  
 ; TITLE OF INVENTION: RILUZOLE  
 ; FILE REFERENCE: 1256-R-00  
 ; CURRENT APPLICATION NUMBER: US/09/892,360  
 ; CURRENT FILING DATE: 2001-06-27  
 ; PRIOR APPLICATION NUMBER: 60/214,559  
 ; PRIOR FILING DATE: 2000-06-27  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1614  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1614)  
 ; OTHER INFORMATION: ORF of human TREK2 cDNA  
 ; US-09-892-360-1

Alignment Scores:

Pred. No.:	3 37e-125	Length:	1614
Score:	1247.50	Matches:	247
Percent Similarity:	78.07%	Conservative:	52
Best Local Similarity:	64.49%	Mismatches:	67
Query Match:	66.25%	Indels:	17
DB:	11	Gaps:	5

US-09-655-272-4 (1-370) x US-09-892-360-1 (1-1614)

Qy	2	AlaAlaProaspLeuLeuaspProlySerAla-----Ala 13
Db	49	GCAGCAGCACCCTGCCAGCCAGCCAGCGCCCAACGGGCAACCCCGGCTCCGGCT 108
Qy	14	GlnAsnSerLysProArgLeuSerPheSerLysProThrValLeuAlaSerArgVal 33
Db	109	CCGACTCAACTCGGCGCTTCTCAITTCCTCCGAGCCACAGTGTAGCC---AGGATG 165
Qy	34	GlusSerAspSer-----AlaIleAsnValMetLysTrpLysThrValSerThrile 50
Db	166	GAAGGCACCTCCCAAGGGGCTTGCAGACCGTCATGAAGTGAAGACGGTGTTCGCATC 225
Qy	51	PheLeuValValLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 70
Db	226	TTTGTGTGTGGTGGTGTACCTGTCTACCTGGCGGTCTTGTCTTCGGGCACTGGAGCAG 285
Qy	71	ProGlnGluLeuSerGlnArgThrThrileValleuGlnLysGlnThrPheIleAlaGln 90
Db	286	CCCTTTGAGACGACCCAGAGAGATACCATCGCTTGGAGAAGCGGAATTCCTCGGGAT 345
Qy	91	HisAlaCysValAsnSerThrGluLeuAspGluLeuGlnGlnValAlaAlaIle 110
Db	346	CATGCTCTGTGAGCCCGCCAGAGCTGGAGACGTTGATCCAGCATGCTCTGTGATGTCGAC 405
Qy	111	AsnAlaGlyIleLeuProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGly 130
Db	406	AAATGGGGAGTCAGTCCCAATAGGAACCTCTCCCAACACAGACGACCACTGGGACCTCGGC 465
Qy	131	SerSerPhePheAlaGlyThrValIleThrThrileGlyPheGlyAsnIleSerPro 150
Db	466	AGTGCCTTTTCTTTGCTGGAACTGTCTATAGCAACATAGGATGATGATGATGCTCCG 525
Qy	151	ArgThrGluGlyGlyLysIlePheCysIleIleTrpAlaLeuLeuGlyIleProLeuPhe 170
Db	526	ACGACTGAAGAGGCAAAATCTTTTGTATTTATATGCACTCTTTGGAAITCCACTCTTT 585
Qy	171	GlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAla 190
Db	586	GGTTTCTTATTGGCTGGAATTTGGAGACCAACTTGGAACTCTTTGGGAAAGCATTTGCA 645
Qy	191	LysValGluAspThrPheIleLysTrpAsnValSerGlnThrLysIleArgIleIleSer 210
Db	646	AGAGTGGGAAGGTCTTTTCGAAAAGACGATGATGATGATGATGATGATGATGATGAT 705
Qy	211	ThrIleIlePheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePhe 230
Db	706	ACCATCTGTTCTATCTTGGCGGCTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 765
Qy	231	LysHisIleGluGlyTrpSerAlaLeuAspAlaIleTrpPheValValIleThrLeuThr 250
Db	766	AAGTACATCAGGCGCTGGAGCGCTTGGAGTCAITTTACTTTTGTGTGTCTACTCTGACC 825
Qy	251	ThrIleGlyPheGlyAspTrpValAlaGlyGly---SerAspIleGluTrpLeuAspPhe 269
Db	826	ACGGTGGGCTTTGGTGATTTTGGTGGGAGGAAACGCTGGCATCAATTTATCGGAGTGG 885
Qy	270	TyrLysProValValTrpPheTrpIleLeuValGlyLeuAlaTrpPheAlaAlaValLeu 289
Db	886	TATAAGCCCTTAGTGTGTTTGGATCTTGTGTGGCTTGTCCCTTACCTTCCAGCTGTCTC 945
Qy	290	SerMetIleGlyAspTrpLeuArgValIleSerLysLysThrLysGluValGlyGlu 309
Db	946	AGTATGATCGGAGATTGGCTACGGGTTCTGTCCAAAAAGACAAAGAGAGGTGGGTGAA 1005

Alignment Scores:

Pred. No.:	3 42e-125	Length:	1632
Score:	1247.50	Matches:	247
Percent Similarity:	78.07%	Conservative:	52
Best Local Similarity:	64.49%	Mismatches:	67
Query Match:	66.25%	Indels:	17
DB:	10	Gaps:	5

US-09-655-272-4 (1-370) x US-09-852-386-34 (1-1632)

Qy	2	AlaAlaProaspLeuLeuaspProlySerAla-----Ala 13
Db	64	GCAGCAGCACCCTGCCAGCGTGTCCAGCCCAAGAGCGCCACTAACGGGCAACCCCGGCTCCGGCT 123
Qy	14	GlnAsnSerLysProArgLeuSerPheSerLysProThrValLeuAlaSerArgVal 33
Db	124	CCGACTCAACTCGGCGCTTGTCCATTTCTCCCGAGCCACAGTGTAGCC---AGGATG 180
Qy	34	GlusSerAspSer-----AlaIleAsnValMetLysTrpLysThrValSerThrile 50



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QY 211 ThrilePheileLeuPheGlyCysValLeuPheValAlaLeuProAlaValilePhe 230
Db 733 ACCATCTGTTCATCTTGGCCGGCTGCATTGTTGTGAGCATCCCTGCTCATCTTT 792
QY 231 LysHileleGluGlyTrpSerAlaLeuAspAlaIleTyPheValValileThrleThr 250
Db 793 AAGTACATCGAGGCTTGGAGCGCTTGGAGTCCATTACTTTGTGTGTCTACTCTGACC 852
QY 251 ThrileGlyPheGlyAspTyPheValAlaGlyGly---SerAspileGluTyPhe 269
Db 853 ACAGTGGGCTTGTGATTTGTGGAGCGGGGAAAGCTGGCATCAATATCGGAGTGG 912
QY 270 TyPheProValValTppPheTppIleLeuValGlyLeuAlaTyPheAlaValleu 289
Db 913 TATAAGCCCTAGTGTGTTTGGATCTTGTGGCTTGTGCTTGTGACGCTGCTCTC 972
QY 290 SerMetileGlyAspTrpLeuArgValileSerIleTyPheValGluValGlyGlu 309
Db 973 AGTATGATCGAGATTCGCTACCGGTTCTGTCCAAAAGACAAAGAGAGTGGTGA 1032
QY 310 PheArgAlaHisAlaAlaGluTppThrAlaAsnValThrAlaGluPheTyPheArg 329
Db 1033 ATCAAGGCCCATCGGAGAGTGGAGGCCAATGTCAAGGCTGAGTTCGGGGAGACAG 1092
QY 330 ArgArgLeuSerValGluIleTyPhePheGlnArgAlaThrSerVal----- 346
Db 1093 CGAAGGCTCAGCTGGAGATCCACGATAAGTGCAGCGGGGAGCCACCATCCGCACATG 1152
QY 347 ---LysArgGlyLeuSerAlaGluLeuAlaGlyAsnHisGlnGluLeuThrProCys 365
Db 1153 GAGCGCGCGGCTGGGCTGGACGAGCGGCCCACTCACTGGACATGCTGTCCCCGAG 1212
QY 366 MetArgThr 368
Db 1213 AAGCGCTCT 1221
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RESULT 9

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US-10-262-511-105
; Sequence 105, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Willet, Isabelle
; APPLICANT: Feyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Wei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
```

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; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Curasequest version 0.1
; SEQ ID NO 105
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(1689)
; US-10-262-511-105

Alignment Scores:
Pred. No.: 4,68e-125 Length: 2028
Score: 1247.50 Matches: 247
Percent Similarity: 78.07% Conservative: 52
Best Local Similarity: 64.49% Mismatches: 67
Query Match: 66.25% Indels: 17
DB: 16 Gaps: 5

US-09-655-272-4 (1-370) x US-10-262-511-105 (1-2028)
QY 2 AlaAlaProAspLeuLeuAspProLysSerAla-----Ala 13
Db 124 GCAGCAGACCCCGTGTGCCAGCCCAAGAGCGCCACTAACGGGCAACCCCGCTCCGCT 183
QY 14 GlnAsnSerLysProArgLeuSerPheSerSerLysProThrValLeuAlaSerArgVal 33
Db 184 CCGACTCCAACTCCGCGCTGTCCATTTCTCCCGAGCCACAGTGGTAGCC---AGGATG 240
QY 34 GluSerAspSer-----AlaIleAsnValMetLysTrpLysThrValSerThrIle 50
Db 241 GAAGGCACCTCCCAAGGGGGCTTGCAGCCGTCATGAGTGAAGACGGTGGTGGCCATC 300
QY 51 PheLeuValValValLeuTyPheLeuIleLeuGlyAlaAlaValPheLysAlaLeuGluGln 70
Db 301 TTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 71 ProGlnGluLeuSerGlnArgThrThrIleValIleGlnLysGlnThrPheIleAlaGln 90
Db 361 CCCTTTGAGAGACGAGCAGAGAAATACCATCGCCCTGGAGAGCGGGAATTCCTGGGGAT 420
QY 91 HisAlaCysValAsnSerThrGluLeuAspGluLeuIleGlnGlnIleValAlaIle 110
Db 421 CATGTCTGTGTGAGCCCCCAGGAGCTGGAGACGCTTCATCCAGCATCTCTTGTGTGTGAC 480
QY 111 AsnAlaGlyIleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGly 130
Db 481 AATCGCGGAGTCAGTCCATAGGAAACTCTTCCAAACACAGCAGCCACTGGGACCTCGGC 540
QY 131 SerSerPhePheAlaGlyThrValIleThrThrIleGlyPheGlyAsnIleSerPro 150
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Db 541 AGTGCCTTTCTTCTGCGAATGTGTCATTTACAGCCATAGGGTATGGGAATATTGCTCCG 600

Qy 151 ArgThrGluGlyGlyLysIlePheCysIleIleTyrAlaLeuLeuGlyIleProLeuPhe 170

Db 601 AGCACTGAAGGAGGCAAAATCTTTTGTATTATATGCAATCTTTTGGAAATTCACATCTTT 660

Qy 171 GlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAla 190

Db 661 GGTTCCTTATTGGCTGGAAATTTGAGAGCAACTTTGGAACCACTTTTGGGAAAAGCATGCA 720

Qy 191 LysValGluAspThrPheIleLysTyrAsnValSerGlnThrLysIleArgIleIleSer 210

Db 721 AGAGTGGAGAGGTCCTTTTCGAAAAGACCAAGTGAATGAGTCAGACCAAGATCCGGGTCACTCTCA 780

Qy 211 ThrIleIlePheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePhe 230

Db 781 ACCATCCTGTTTCATCTTTGGCGGCTGCTATTGTGTTGTGACGATCCCTGCTGTCACTTT 840

Qy 231 LysHisIleGluGlyTyrSerAlaLeuAspAlaIleTyrPheValValIleThrLeuThr 250

Db 841 AAGTACATCATGAGGCTGAGCGGCTTTGGAGTCCATTTACTTTGTGTGTGTCATCTTGACC 900

Qy 251 ThrIleGlyPheGlyAspTyrValAlaGlyGly--SerAspIleGluTyrLeuAspPhe 269

Db 901 ACGGTGGGCTTTGCTGATTTTTTTTGTGGCAGGGGAAACGCTGGCATCAATTATCGGGAGTGG 960

Qy 270 TyrLysProValValTyrPheTyrIleLeuValGlyLeuAlaTyrPheAlaAlaValLeu 289

Db 961 TATAAGCCCTAGTGTGTTTGGATCTTGTGTGGCTTGCCTACTTTGCAGCTGTCTCTC 1020

Qy 290 SerMetIleGlyAspTyrLeuArgValIleSerLysLysThrLysGluValGlyGlu 309

Db 1021 AGTATGATCGAGATGGCTACGGGTTCTGTCCAAAAAGACAAAAGAGAGGTGGGTGAA 1080

Qy 310 PheArgAlaHisAlaAlaGluTyrThrAlaAsnValThrAlaGluPheLysGluThrArg 329

Db 1081 ATCAAGGCCCATCGGCAGAGTGAAGGCCAATGTCAACGCTGAGTTCGGGAGACACGG 1140

Qy 330 ArgArgLeuSerValGluIleTyrAspLysPheGlnArgAlaThrSerVal----- 346

Db 1141 CGAAGGCTCAGCTGGAGATCCAGTATAGCTCAGCGGGGGCCACCATCCGCAGCATG 1200

Qy 347 ---LysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrProCys 365

Db 1201 GAGCGCGCGGCTGGGCTGGACCGGCGCCACTCATGTGACATGCTGTCCCCCGAG 1260

Qy 366 MetArgThr 368

Db 1261 AAGCGCTCT 1269

RESULT 10

US-09-729-920-1

; Sequence 1, Application US/09729920

; Patent No. US20020103115A1

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS.

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000088

; CURRENT APPLICATION NUMBER: US/09/729, 920

; CURRENT FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2065

; TYPE: DNA

; ORGANISM: Human

US-09-729-920-1

Alignment Scores: 4.8e-125 Length: 2065

Pred. No.: 1247.50 Matches: 247

Score:



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Db      1454 ATCAAGGCCCATGCGGCAGAGTGAAGGCCAATGTACGGCTGAGTTCGCGAGACACGG 1513
Qy      330 ArgArgLeuSerValGluIleTyrAspLysPheGlnArgAlaThrSerVal----- 346
Db      1514 CGAAGGCTCAGCGTGAGATCCACGATAGCTGCAGCGCGGCCACCATCCGACGATG 1573
Qy      347 ---LysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrProCys 365
Db      1574 GAGCGCGCGGCTGGCGCTGGACCGAGCGGCCCACTACTGACATGCTGTCCCCCGAG 1633
Qy      366 MetArgThr 368
Db      1634 AAGCGCTCT 1642

RESULT 11
US-10-887-932-1
; Sequence 1, Application US/10887932
; Publication No. US20040247595A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USE THEREOF
; FILE REFERENCE: CLO00858
; CURRENT APPLICATION NUMBER: US/10/887,932
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2065
; TYPE: DNA
; ORGANISM: Human
US-10-887-932-1

Alignment Scores:
Pred. No.:      4, 8e-125      Length:      2065
Score:          1247.50      Matches:      247
Percent Similarity: 78.07%      Conservative: 52
Best Local Similarity: 64.49%      Mismatches: 67
Query Match:      66.25%      Indels:      17
DB:              18          Gaps:       5

US-09-655-272-4 (1-370) x US-10-887-932-1 (1-2065)
Qy      2 AlaAlaProAspLeuAspProLysSerAla-----Ala 13
Db      497 GCAGCAGCAGCCGGTGTGCAGCCCAAGAGCGCCACTAAGCGGCACCCCGGCTCCGGCT 556
Qy      14 GlnAsnSerLysProArgLeuSerPheSerLysProThrValLeuAlaSerArgVal 33
Db      557 CCGACTCCAACTCCGGCGCTGTCCATTCTCTCCGAGGCCACAGTGGTAGCC---AGGATG 613
Qy      34 GluSerAspSer-----AlaLeuValMetLysThrLysThrValSerThrIle 50
Db      614 GAAGGCACCTCCCAAGGGGGCTTGCAGACCGTCATGAAGTGAAGACCGTGGTGGCCATC 673
Qy      51 PheLeuValValLeuTyrLeuIleGlyAlaAlaValPheLysAlaLeuGluGln 70
Db      674 TTGTGGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 733
Qy      71 ProGlnGluLysSerGlnArgThrThrIleValIleGlnLysGlnThrPheIleAlaGln 90
Db      734 CCCTTTGAGAGCAGCCAGAGAAATACCATCGCTTGGAGAGCGCGAAATCTCGCGGAT 793
Qy      91 HisAlaCysValAsnSerThrGluLeuAspGluLeuIleGlnGlnIleValAlaAlaIle 110
Db      794 CATGTCTGTGTGAGCCCCAGGAGCTGGAGACGTTGATCCAGCATGCTCTTGTATGCTGAC 853
Qy      111 AsnAlaGlyIleIleProLeuGlyAsnSerSerAsnGlnValSerHisThrAspLeuGly 130
Db      854 AATCGGGAGTCACTCCAAATAGGAACTCTTCCAAACACAGCAGCCACTGGGACCTCGGC 913
Qy      131 SerSerPhePheAlaGlyThrValIleThrIleGlyPheGlyAsnIleSerPro 150

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Db      914 AGTGCCTTTTCTTCTGCAACTGTCTAGCACCATTAGGAGTATGGGAATATGCTCCG 973
Qy      151 ArgThrGluGlyGlyLysLysPheCysIleIleTyrAlaLeuGluLysLeuPhe 170
Db      974 AGCACTGAAGGAGGCAAAATCTTTTGTATTTATATGCCATCTTTGGAAATCCACTCTTT 1033
Qy      171 GlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAla 190
Db      1034 GGTTTCTTATGCTGGATTGGAGAACCACTTGGAAACCATCTTTGGGAAAAAGCATGCA 1093
Qy      191 LysValGluAspThrPheIleLysTyrAsnValSerGlnThrLysIleArgIleLeuSer 210
Db      1094 AGAGTGAGAGAGGTCTTTTCGAAAAAAGCAAGTGAGTCAGACCAAGATCCGGTCATCTCA 1153
Qy      211 ThrIleIlePheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePhe 230
Db      1154 ACCATCTCTGTTCATCTTGGCGGCTGTCATGTGTGTGTGACGATCCTGCTGTCATCTTT 1213
Qy      231 LysHisIleGluGlyTyrSerAlaLeuAspAlaIleTyrPheValValIleThrLeuThr 250
Db      1214 AAGTACATCGAGGCTGAGCGCTTGGAGTCCATTTACTTTTGTGGTGGTCACTCTGACC 1273
Qy      251 ThrIleGlyPheGlyAspTyrValAlaGlyGly---SerAspIleGluTyrLeuAspPhe 269
Db      1274 ACGTGGGCTTGTGTGATTTTGTGGCAGGGGAAACGCTGCGCATCAATTATCGGAGTGG 1333
Qy      270 TyrLysProValValTyrPheTyrPheIleLeuValGlyLeuAlaTyrPheAlaAlaValLeu 289
Db      1334 TATAAGCCCTAGTGTGTGTGTGATCCTTGTGGCTTGCCTACTTTGAGCTGTCTC 1393
Qy      290 SerMetIleGlyAspTyrLeuArgValIleSerLysLysThrLysGluGluValGlyGlu 309
Db      1394 ACTATGATCGAGATTTGGCTACGGGTCTGTGCAAAAAGACAAAGAGAGGTGGGTGAA 1453
Qy      310 PheArgAlaHisAlaAlaGluTyrThrAlaAsnValThrAlaGluPheLysGluThrArg 329
Db      1454 ATCAAGGCCCATTCGCGAGAGTGGAGGCCAATGTCACGGCTGAGTTCGCGAGACACGG 1513
Qy      330 ArgArgLeuSerValGluIleTyrAspLysPheGlnArgAlaThrSerVal----- 346
Db      1514 CGAAGGCTCAGCGTGGAGATCCAGATAAGTGCAGCGGGCGGCCACCATCCGAGCATG 1573
Qy      347 ---LysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrProCys 365
Db      1574 GAGCGCGCGGCTGGCGCTGGACCGAGCGGCCCACTACTGAGCATGCTGTCCCCCGAG 1633
Qy      366 MetArgThr 368
Db      1634 AAGCGCTCT 1642

RESULT 12
US-10-302-172-432
; Sequence 432, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; TITLE OF INVENTION: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803 1CNCp
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pc_FL_genes Version 2.0
; SEQ ID NO 432

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; LENGTH: 2730
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (473)..(2086)
US-10-302-172-432

Alignment Scores:
Pred. No.: 7,19e-125 Length: 2730
Score: 1247.50 Matches: 247
Percent Similarity: 78.07% Conservative: 52
Best Local Similarity: 64.49% Mismatches: 67
Query Match: 66.25% Indels: 17
DB: 16 Gaps: 5

US-09-655-272-4 (1-370) x US-10-302-172-432 (1-2730)

QY 2 AlaAlaProAspLeuLeuAspProLysSerAla-----Ala 13
DB 521 GCAGCAGCACCGGTGTGCCAGCCCAAGAGCGCCACTTAACGGGCAACCCCGGCTCCGGCT 580
QY 14 GlnAsnSerLysProArgLeuSerPheSerSerLysProThrValLeuAlaSerArgVal 33
DB 581 CCGACTCCAACCTCGCGCCCTGTCCATTCTCCGAGCCACAGTGTAGCC--AGGATG 637
QY 34 GluSerAspSer-----AlaAlaAsnValMetLysTrpLysThrValSerThrile 50
DB 638 GAAGGCACCTCCCAAGGGGCTTGCAGACCGTCTCATGAAGTGAAGACCGTGTGTCATC 697
QY 51 PheLeuValValValLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeu 70
DB 698 TTTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 757
QY 71 ProGlnGluLeuSerGlnArgThrThrIleValIleGlnLysGlnThrPheIleAlaGln 90
DB 758 CCTTTGAGAGCAGCCAGAGAAATACCATCGCTTGGAGAGCGGAAATTCCTCGCGGAT 817
QY 91 HisAlaCysValAsnSerThrGluLeuAspGluLeuGlnGlnIleValAlaAlaIle 110
DB 818 CATGCTGTGTGTGAGCCCGGAGGAGTGTGAGACGTTGATCCAGCATGCTCTGTATGCTGAC 877
QY 111 AsnAlaGlyLeuLeuProLeuGlyValAsnSerSerAsnGlnValSerHisTrpAspLeuGly 130
DB 878 AATGCGGAGTCACTCCATAGGAAATCTTCCAAACACAGCAGCCACCTGGGACCTCGGC 937
QY 131 SerSerPhePheAlaGlyThrValIleThrThrIleGlyPheGlyAsnIleSerPro 150
DB 938 AGTGCCCTTTTCTTGTGCTGAACTGTCTATACGACCATAGGGTATGGAAATATGCTCCG 997
QY 151 ArgThrGluGlyGlyLysIlePheCysIleIleIleIleIleIleIleIleIleIleIle 170
DB 998 AGCACTGAAGGAGGCAAAATCTTTGTATTATATATATATATATATATATATATATATAT 1057
QY 171 GlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAla 190
DB 1058 GGTTCCTTATTGTGGAATTGGAGACCAACTTGGAAACCATCTTTGGGAAAGCAATTGCA 1117
QY 191 LysValGluAspThrPheIleLysTrpAsnValSerGlnThrLysIleArgIleIleSer 210
DB 1118 AGAGTGAGAGAGTCTTTCGAAAAGCAAGTGCAGACCAAGATCCGGGTCATCTCA 1177
QY 211 ThrIleIlePheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePhe 230
DB 1178 ACCATCTGTTCATCTTGGCGGCTGCATGTGTGTGTGACGATCCCTGTGTGTGTGTGT 1237
QY 231 LysHisIleGluGlyTrpSerAlaLeuAspAlaIleTrpPheValValIleThrLeuThr 250
DB 1238 AAGTATCATCAGGCGCTGCAGCGGCTTGGAGTCCATTACTTTGTGTGTGTGTGTGTGTGT 1297
QY 251 ThrIleGlyPheGlyAspTrpValAlaGlyGly---SerAspIleGluTrpLeuAspPhe 269
DB 1298 ACGGTGGGCTTTGGTATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1357
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270 TyrLysProValValTrpPheTrpIleLeuValGlyLeuAlaTyrPheAlaAlaValLeu 289
1358 TATAAGCCCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1417
QY 290 SerMetIleGlyAspTrpLeuArgValIleSerLysLysThrLysGluGluValGlyGlu 309
1418 AGTATGATCGGAGATTGGCTACGGGTTCTGTCCAAAAGACAAAGAGAGGTGGGTGAA 1477
QY 310 PheArgAlaHisAlaAlaGluTrpThrAlaAsnValThrAlaGluPheLysGluThrArg 329
1478 ATCAAGGCCCATGCGGAGAGTGAAGGCCAATGTCAAGGCTGAGTTCGGGAGACACGG 1537
QY 330 ArgArgLeuSerValGluIleTyrAspLysPheGlnArgAlaThrSerVal----- 346
1538 CGAAGGCTCAGCGTGGAGATCCACGATAAGCTCAGCGGGCGGCCACCATCCGAGCATG 1597
QY 347 ---LysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrProCys 365
1598 GACGCGCGGCGCTGGGCTGGACGAGCGGGGCCACTCACTGGACATGCTGTCCCCCGAG 1657
QY 366 MetArgThr 368
1658 AAGCGCTCT 1666

RESULT 13
US-10-332-447-42
; Sequence 42, Application US/10332447
; Publication No. US20040053258A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; RAUMANN, Brigitte E.;
; APPLICANT: THORNTON, Michael; DING, Li; YUB, Henry;
; APPLICANT: TANG, Y.Tom; HARLAND, Lee; BURFORD, Neil;
; APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;
; APPLICANT: RAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;
; APPLICANT: ARVIZU, Chandra S.; GANDHI, Ameena R.;
; APPLICANT: HAFALIA, April J.A.; TRIBOULEY, Catherine M.;
; APPLICANT: WALIA, Narinder K.; AU-YOUNG, Janice;
; APPLICANT: WALSH, Roderick T.; RAMKUMAR, Jayalaxmi;
; APPLICANT: LU, Yan; LU, Dyung Aina M.; AZIMZAI, Yalda;
; APPLICANT: LAL, Preeti; ELLIOTT, Vicki S.; NGUYEN, Dannel B.;
; APPLICANT: XU, Yuming; SEILHAMER, Jeffrey J.; BOROWSKY, Mark L.;
; APPLICANT: KHAN, Farran A.; KEARNEY, Liam; THANGAVELU, Kavitha;
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0149 USN
; CURRENT APPLICATION NUMBER: US/10/332,447
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/216,547
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/218,232
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,112
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/221,839
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PERL Program
; SEQ ID NO 42
; LENGTH: 2820
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053258A1 7472728CB1
US-10-332-447-42

Alignment Scores:
Pred. No.: 7,33e-122 Length: 2820
Score: 1220.00 Matches: 244
Percent Similarity: 76.74% Conservative: 53
Best Local Similarity: 63.05% Mismatches: 68
Query Match: 64.79% Indels: 22
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DB:	16	Gaps:	6
US-09-655-272-4 (1-370) x US-10-332-447-42 (1-2820)			
QY	2	AlaAlaProAspLeuLeuAaspProIysSerAla-----Ala 13	
DB	598	GCAGCAGCAGCGGTGTGCCAGGCCAAGAGCCACATAACGGGCAACCCCGGCTCCGGCT 657	
QY	14	GlnAsnSerIysProArgLeuSerPheSerLysProThrValLeuAlaSerArgVal 33	
DB	658	CCGACTCCAACTCCGGCGCTGTCCATTCTCCGAGCCACAGTGTAGCC---AGGATG 714	
QY	34	GluSerAspSer-----AlaIleAsnValMetLysTrpLysThrValSerThrIle 50	
DB	715	GAAGGCACCTCCCAAGGGGCTTGCAGACCGTCATGAAGTGAAGACGGTGTGCCATC 774	
QY	51	PheLeuValValValLeuLysLeuIleGlyAlaAlaValPheLysAlaLeuGluGln 70	
DB	775	TTTGTGTTGTGTGTGTACCTTGTACCTGCGGCTTGTCTTCGGGCATTTGGAGCAG 834	
QY	71	ProGlnGluIleSerGlnArgThrIleValIleGlnLysGlnThrPheIleAlaGln 90	
DB	835	CCCTTGAGAGCCGAGAGATACCATCGCTTGGAGAGCGGAATTCCTGCGGGAT 894	
QY	91	HisAlaCysValAsnSerThrGluLeuAspGluLeuIleGlnIleValAlaIle 110	
DB	895	CATGCTGTGTGAGCCGCCAGGAGCTGGAGACGTTGATCCAGCATGCTCTTGATGCTGAC 954	
QY	111	AsnAlaGlyIleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGly 130	
DB	955	AATCGGGAGTCAGTCCNATAGGAACCTCTTCCACAAACAGCAGCCATGGGACCTCGGC 1014	
QY	131	SerSerPhePheAlaGlyThrValIleThrThrIleGlyPheGlyAsnIleSerPro 150	
DB	1015	AGTGCTTTTCTTGTGCGAATGTATTACGACCATG---TATGGGAATATGTCTCG 1071	
QY	151	ArgThrGluGlyGlyValIlePheCysIleIleValAlaLeuLeuGlyIleProLeuPhe 170	
DB	1072	AGCATGTAAGAGGGAATCTTTTGTATTTATATGCTATGCTTTTGGAAATTCACCTCTT 1131	
QY	171	GlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAla 190	
DB	1132	GCTTTCTATTGCTGGAATTTGGAGCAACTTGGAACTTGTGGAAAGCATTTGCA 1191	
QY	191	LysValGluAspThrPheIleLysTrpAsnValSerGlnThrLysIleArgIleIleSer 210	
DB	1192	AGAGTGGAGAGGTCTTTTCGAAAAAGCAAGTGAAGTCAACAGATCCGGTCACTCA 1251	
QY	211	ThrIleIlePheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePhe 230	
DB	1252	ACATCTCTTTTCTTGTGCGCGCTGCTATGTTGTGAGCATCCCTGCTGTCTATCTTT 1311	
QY	231	LysHisIleGluGlyTrpSerAlaLeuAspAlaIleValPheValValIleThrLeuThr 250	
DB	1312	NAGTACATCGAGGCTTGGAGCGCTTGGAGTCCATTACTTTTGTGTGTGTCACTCTGACC 1371	
QY	251	ThrIleGlyPheGlyAspThrValAla-----GlyGlySerAspIleGlu 265	
DB	1372	ACGGTGGGCTTTGGTGATTTTGTGGCAGTGTGTTTTCAGGGGAAACGCTGGCATCAAT 1431	
QY	266	TyrLeuAspPheThrLysProValValTrpPheTrpIleLeuValGlyLeuAlaThrPhe 285	
DB	1432	TATCGGAGTGGGTATAAGCCCTTAGTGTGTTTGGATCTTGTGTGGCTTGCCTACTTT 1491	
QY	286	AlaAlaValLeuSerMetIleGlyAspTrpLeuAlaValIleSerLysLysThrLysGlu 305	
DB	1492	GCAGCTGTCTCAGTATGATCGGAGATTGGCTACGGTCTGTCCAAAAAGACAAAGAA 1551	
QY	306	GluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsnValThrAlaGluPhe 325	
DB	1552	GAGTGGTGAATCAAGGCCCATGCGCAGAGTGAAGCCAATGTCACTGAGTTC 1611	
QY	326	LysGluThrArgArgLeuSerValGluIleThrAspLysPheGlnArgAlaThrSer 345	

DB	1612	CGGAGACACGGCGAAGGCTCAGCGTGGAGATCCAGATAAGCTCAGCGGCGACCCACC 1671	
QY	346	Val-----LysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGlu 361	
DB	1672	ATCCGAGCATGAGAGCGCGGCGGTGGGCTTGGACCGAGCGGCCCACTCACTGGACATG 1731	
QY	362	LeuThrProCysMetArgThr 368	
DB	1732	CTGTCCCGGAGAGCGCTCT 1752	
RESULT 14			
US-10-243-035-1			
Sequence 1, Application US/10243035			
Publication No. US20030049697A1			
GENERAL INFORMATION:			
APPLICANT: LAZDUNSKI, MICHEL			
APPLICANT: LESAGE, FLORIAN			
APPLICANT: MAINGRET, FRANCOIS			
TITLE OF INVENTION: NEW FAMILY OF MECHANOSENSITIVE HUMAN POTASSIUM CHANNELS			
TITLE OF INVENTION: ACTIVATED BY POLYUNSATURATED FATTY ACIDS AND THEIR USE			
FILE REFERENCE: 1317-02			
CURRENT APPLICATION NUMBER: US/10/243,035			
CURRENT FILING DATE: 2002-09-13			
NUMBER OF SEQ ID NOS: 15			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 1			
LENGTH: 1182			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1)..(1179)			
US-10-243-035-1			
Alignment Scores:			
Pred. No.:	1,956-76	Length:	1182
Score:	797.00	Matches:	145
Percent Similarity:	72.18%	Conservative:	60
Best Local Similarity:	51.06%	Mismatches:	77
Query Match:	42.33%	Indels:	2
DB:	14	Gaps:	1
US-09-655-272-4 (1-370) x US-10-243-035-1 (1-1182)			
QY	42	MetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuValLeuVal 61	
DB	1	ATCGCAGCACCACTCTCTGCGCTCTGCGCTCTGCGCTCTGCTTACTTGTGTCTGT 60	
QY	62	AlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIleVal 81	
DB	61	GCCTGTGTTCGGGCTCTGGAGCAGCCCGCAGCAGCAGCAGCAGCAGCAGCAGCAG 120	
QY	82	IleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAspGlu 101	
DB	121	GAGGTCCGAGAGAAATCTCTGAGGCGCCATCCGTGTGTGAGCAGCAGCAGCAGCAG 180	
QY	102	LeuIleGlnIleValAlaIleAsnAlaGlyIleIleProLeuGlyAsnSerSer 121	
DB	181	CTCATAGAGAGTGGCTGATGCCCTGGGAGGGGTGGGACCCAGAAACCACTCGACC 240	
QY	122	AsnGlnValSerHis-----TrpAspLeuGlySerSerPhePheAlaGlyThrVal 139	
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QY	140	IleThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCys 159	
DB	301	ATCACCACTCGCTATGGCAATGTGGCCCTCGCAGACAGATGCCGGCGCTCTTCTGC 360	
QY	160	IleIleValAlaLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsp 179	
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QY 180 GlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTyr 199
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QY 200 AsnValSerGlnThrLysIleArgIleSerThrIlePheIleLeuPheGlyCys 219
Db 481 CAGTGCACCGGAGCTAGTAAGAGTGTCTGGCGATGTTCTTCTGCTGATCGGCTGC 540
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QY 260 GlyClySerAspIleGluTyrLeuAspPheTyrLysProValValTyrPheTyrIleLeu 279
Db 661 GGCGCGACCCAGGAGGACTCCCGGCTATCAGCCGCTGTGTGTGTCTGATCCTG 720
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QY 320 AsnValThrAla 323
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## RESULT 15

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; Patent No. US20020034781A1
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; TITLE OF INVENTION: 12303, A NOVEL HUMAN TWIK MOLECULE AND USES THEREOF
; FILE REFERENCE: WNI-142
; CURRENT APPLICATION NUMBER: US/09/828,035
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,734
; PRIOR FILING DATE: 2000-04-07
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; FEATURE:
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; LOCATION: (1)..(1257)
US-09-828-035-3
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US-09-655-272-4 (1-370) x US-09-828-035-3 (1-1257)

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QY 140 IleThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCys 159
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QY 160 IleIleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsp 179
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 22:13:21 ; Search time 4470.83 Seconds  
(without alignments)  
3355.931 Million cell updates/sec

Title: US-09-655-272-4

Perfect score: 1883

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Listing first 45 summaries

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 ; APPLICANT: Conrad Gerald Chapman  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP-30031-D1  
 ; CURRENT APPLICATION NUMBER: US/09/828,746  
 ; CURRENT FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 09/236,080  
 ; PRIOR FILING DATE: 1999-01-25  
 ; PRIOR APPLICATION NUMBER: EP 98300570.3  
 ; PRIOR FILING DATE: 1998-01-27  
 ; PRIOR APPLICATION NUMBER: UK 9822135.1  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1994  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 US-09-828-746-5

Alignment Scores:  
 Pred. No.: 3.1e-197 Length: 1994  
 Score: 1870.00 Matches: 368  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.31% Indels: 0  
 DB: 34 Gaps: 0

US-09-655-272-4 (1-370) x US-09-828-746-5 (1-1994)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 DB 484 ATGGCGGCGCCCTGACTTGTGGATCCAGTCTGCTCAGAACTCCAAACCGAGGCTC 543  
 QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 DB 544 TCATTCTCTTCAAAACCCACCGTGTCTTCCGGGTGGAGAGTACTCGGCCATTAT 603  
 QY 41 ValMetLysTriLysThrValSerThrIlePheLeuValValLeuThrIleIle 60  
 DB 604 GTTATCAAAATGGAGACAGTCTCCACGATTTTCCTGGTGGTCTCTTACCTGATCATC 663  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
 DB 664 GGAGCGCGCGGTGTTCAGGCATTTGGAGAGCCCTCAGAGATTTCCAGAGGACCACCAIT 723  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 784 GAACATCATCCAGCAATAGTGGCAGCAATAAACCGAGGATTTATCCCTTAGGAACAGC 843  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 DB 844 TCCAAATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTTCTTCTTCTTCTTCTTATC 903  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160



```
Db 904 ACAACCATGAGTTGGAAACATCTCCCAACGAACTCAAGAGTGGAAATATTTCTGCATC 963
Qy 161 ILeTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 964 ATCTATGCTTGTGGGAATCCCTCTTTGGCTTCTACTGGCTGGGTGGTGATCAG 1023
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 1024 CTAGGAATATATTTGGAAAGAAATTCGCAAGTGGAAACACATTTATTAAGTGAAT 1083
Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 1084 GTTAGTCAGACGAGATTCGTATCATCTCCACCATCATCTTCATCCTGTTGGCTGGTC 1143
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 1144 CTCTTTGGCTCTCCCTCGGTCATATTCAGCACATAGAGGCTGGAGCGCCCTGGAC 1203
Qy 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 1204 GCTATCTATTTGTGGTTATCACTCTGACGACCATTCGATTTGGAGACTACGTGGCAGGT 1263
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 1264 GGAATCAGACATGAATATCTGGACTTCTACAGCCTGTGGTGTCTGGATCCTCGTT 1323
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 1324 GGCTGGCTTACTTTGAGCTGTCTGAGCATGATTTGGGACTGGCTACGGGTGATCTCT 1383
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 1384 AAGAAGCAAGGAAGAGGTGGGAGCTTCAGAGCGCATGCCGTGAGTGGACAGCCAAAT 1443
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 1444 GTCACGGCCGAGTTTCAAGGAACGAGGAGCGGCTGAGCGTGAGATCTACGCAAGTTC 1503
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1504 CAGGTGGCCATCCCTGAGCGGAGCTCTCCGACAGCTGGCGGCGCAACCAACACAG 1563
Qy 361 GluLeuThrProCysMetArgThr 368
Db 1564 GAACTGACTCCGTGTATGAGGACC 1587
```

## RESULT 2

```
US-10-036-657-37
; Sequence 37, Application US/10036657
; GENERAL INFORMATION:
; APPLICANT: Earl Francis Albone, et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: GP-70778B-C1
; CURRENT APPLICATION NUMBER: US/10/036,657
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-036-657-37
```

```
Alignment Scores:
Pred. No.: 3,1e-197 Length: 1994
Score: 1870.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.31% Indels: 0
DB: 45 Gaps: 0
```

US-09-655-272-4 (1-370) x US-10-036-657-37 (1-1994)

```
Qy 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 484 ATGGCGGCCCTGACTTGTCTGGATCCCAAGTCTGCTCAGAACTCCAAACCGAGGCTC 543
Qy 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 544 TCATTCTCTTCAAAACCCACCGCTGCTTCCCGGTGGAGAGTGACTCGGCCATTAAT 603
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrLeuIleIle 60
Db 604 GTTATGAATGGAAGACAGCTCTCCAGATTTCTTGGTGGCTGCTCTTACCTGATCATC 663
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLysSerGlnArgThrThrIle 80
Db 664 GGAGCGCGGTGTTCAGGCAATTTGGAGCAGCTTCAGAGATTTCCCGAGAGCACCATTT 723
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 724 GTGATCCAGAAAGCAGACCTTCATAGCCCGAGCATGCCCTGGCTCAACTCCACCGAGCTGGAC 783
Qy 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 784 GAACTCATCCAGCAATATAGTGGCAGCANTAAACGAGGGATTAATCCCTTAGGAACAGC 843
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 844 TCCAAATCAAGTAGTCACTGGGACCTCGGAAGCTCTTCTCTTCTGCTGTACTGTATC 903
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160
Db 904 ACAACATATAGGATTTGGAACAATCTCCCAACGAATCAAGGTGGAAAAATATTTCTGCATC 963
Qy 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 964 ATCTATGCTTGTCTGGGAATTCCTCTTGGCTTCTACTGGCTGGGTGGTGATCAG 1023
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 1024 CTAGGAATATATTTGGAAAGAAATTCGCAAGTGGAAACACATTTATTAAGTGAAT 1083
Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 1084 GTTAGTCAGACGAGATTCGTATCATCTCCACCATCATCTTCATCCTGTTGGCTGGTC 1143
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 1144 CTCTTTGGCTCTCCCTCGGTCATATTCAGCACATAGAGGCTGGAGCGCCCTGGAC 1203
Qy 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 1204 GCTATCTATTTGTGGTTATCACTCTGACGACCATTTGGATTTGGAGACTACGTGGCAGGT 1263
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 1264 GGATCAGACATGAATATCTGGACTTCTACAAACCTGTGGTGGTCTGGATCCTCGTT 1323
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 1324 GGGCTGGCTTACTTTGACGCTGTTCTGAGCATGATTTGGGACTGGCTACGGGTGATCTCT 1383
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 1384 AAGAAGCAAGGAAGAGGTGGGAGGTTCAGAGCGCATGCCGTGAGTGGACAGCCAAAT 1443
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 1444 GTCACGGCCGAGTTTCAAGGAACGAGGAGCGGCTGAGCGTGAGATCTACGCAAGTTC 1503
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1504 CAGGTGGCCATCCGTGAGCGGAGCTCTCCGACAGCTGGCGGCGCAACCAACACAG 1563
```



US-09-655-272-4 (1-370) x US-09-503-089A-1 (1-1236)

```
QY 1 MetAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 1 ATGGCGGCCCTGACTGCTGGATCCTAAATCTGCGCTCAGAACTCCAAACCGAGGCTC 60
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 61 TCGTTTTCCAGAAACCCACAGTGTCTTCCCGGTGGAGAGTGACACGACCATTAAT 120
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrLeuIleIle 60
Db 121 GTTATGAAATGGAGACGGTCTCAGATATTCCTGGTGTCTCAATCTTAICTGATCATC 180
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrThrIle 80
Db 181 GGAGCCACCGTGTTCAGAACATTTGGAGCAGCCTCATGAGATTTTCACAGAGGACCCATT 240
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 241 GTGATCCAGAACCAACATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 300
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 301 GAACATTCATCAGCAATAGTGGCAGCAATTAATGACGGATTAATCCGTTAGGAACACC 360
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 361 TCCAATCAATCAGTCAGTGGATTTGGGAAGTTCCTTCTTCTTGTGGCACTGTTATT 420
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160
Db 421 ACAACCATAGGATTTGGAAACATCTCACCAACGACAGAGCGGCAAAATATTTCTGTATC 480
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180
Db 481 ATCTATGCCCTTACTGGAAATCCCTCTTTGGTTTTCTCTTGGCTGGAGTTGGAGATCAG 540
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 541 CTAGGCACCATATTTGGAAAGGAATGCCAAGTGGAGATACGTTTATTAAGTGGAAAT 600
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 601 GTTAGTCAGACCAAGATTCGCATCATCTCAACATCATATTTATATCTATTGTGCTGTGA 660
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 661 CTCTTTGTGGCTCTGCCCTGGATCATATTCAAACATAGAAAGCTGGAGTGCCTGGAC 720
QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 721 GCCATTTATTTTGGTTATCACTCTAACCACTATTGGATTTGGTACCTAGCTTGAGGT 780
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 781 GGATCCGATATCAATATCTGGACTTCTATAAGCCTGTCTGTGGTTCTGGATCCTTGTA 840
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 841 GGGCTTGTCTTACTTGTCTGCTGCTGAGATGATTTGGAGATTTGGCTCCGAGTGATCT 900
QY 301 LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 901 AAAAGACAAAAGAGGTTGGAGAGTTTCAGAGCACACGCTCTCTGAGTGGACAGCCAAC 960
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 961 GTCACAGCCGAATTCAAAGAAACAGGAGCGAGTGTGAGATTTATGACAAAGTTC 1020
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1021 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGCAGAACTGGCTGGAAACCAATCAG 1080
```

```
QY 361 GluLeuThrProCysMetArgThr 368
Db 1081 GAGTCGACTCCTTGTAGGAGGACC 1104
```

## RESULT 5

```
US-09-828-746-1
; Sequence 1, Application US/09828746
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1246
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-828-746-1
```

## Alignment Scores:

```
Pred. No.: 2,216-193 Length: 1246
Score: 1833.00 Matches: 356
Percent Similarity: 98.91% Conservative: 8
Best Local Similarity: 96.74% Mismatches: 4
Query Match: 97.34% Indels: 0
DB: 34 Gaps: 0
```

US-09-655-272-4 (1-370) x US-09-828-746-1 (1-1246)

```
QY 1 MetAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 9 ATGGCGGCCCTGACTGCTGGATCCTAAATCTGCGCTCAGAACTCCAAACCGAGGCTC 68
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 69 TCGTTTTCCAGAAACCCACAGTGTCTTCCCGGTGGAGAGTGACACGACCATTAAT 128
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrLeuIleIle 60
Db 129 GTTATGAAATGGAGACGGTCTCCACGATATTCTCTGGTGTGTCTCTATCTGATCATC 188
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrThrIle 80
Db 189 GGAGCCACCGTGTTCAGAACATTTGGAGCAGCCTCATGAGATTTTCAGAGGACCCATT 248
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 249 GTGATCCAGAACCAACATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 308
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 309 GAACATTCATTCAGCAATAGTGGCAGCAATTAATGACGGATTAATCCGTTAGGAACACC 368
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 369 TCCAATCAATCAGTCAGTGGATTTGGAGAGTTCCTTCTTCTTGTGGCACTGTTATT 428
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160
Db 429 ACAACCATAGGATTTGGAAACATCTCACCAACGACAGAGGCGGCAAAATATTTCTGTATC 488
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180
```

489 ATCTATGCTTACTGGGAATCCCTCTTTGGTTTCTTTGGCTGGAGTTGGAGATCAG 548  
181 LeuGlyThrThrLeuPheGlyValAlaGlyValGluAspThrPheLeuLeuValAsn 200  
549 CTAGGCACCAATTTGGAAAGGAATTCGAAGTGGAGATACGTTTATTAAAGTGAAT 608  
201 ValSerGlnThrLysLeuArgLeuLeuSerThrLeuLeuPheLeuPheGlyCysVal 220  
609 GTTAGTCAGACCAAGATTGCATCATCTCAACAATCATATTTATATCTTTGGCTGTGTA 668  
221 LeuPheValAlaLeuProAlaValLeuPheLeuHisLeuGluCysThrSerAlaLeuAsp 240  
669 CTCCTTTGGCTCTGGCTGGATCATATTCACAACATAGAGGCTGGAGTGCCTGGAC 728  
241 AlaLeuThrPheValValLeuThrLeuThrThrLeuGlyPheGlyAspTyrValAlaGly 260  
729 GCCATTTATTTTGGTTATCACTCTCAACAATCATTTGGATTTGGTACCTTGCAGGT 788  
261 GlySerAspLeuGluThrLeuAspPheTyrLysProValValThrPheThrLeuVal 280  
789 GGATCCGATATTGAATATCTGGATCTCTATAAGCCTGTGTGGTTCTGGATCTTGTGA 848  
281 GlyLeuAlaThrPheAlaAlaValLeuSerMetIleGlyAspThrLeuArgValIleSer 300  
849 GGGCTTGCCTTACTTTGCTGCTGCTGAGCATGATTGGAGTTGGCTCCGAGTGATATCT 908  
301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluThrAlaAsn 320  
909 AAAAAGACAAAGAGAGTGGAGAGTTCCAGAGCACACCTCTGAGTGGACAGCAAC 968  
321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluLeuLeuThrAspLysPhe 340  
969 GTACAGCCGAATTCNAAGAAACAGAGGCGAGTGGAGTGGAGATTATGACAAAGTTC 1028  
341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
1029 CAGGGGCCACTCCATCAGCGAGCTCTGGCAGAACTGGCTGGAAACCAATCAG 1088  
361 GluLeuThrProCysMetArgThr 368  
1089 GAGCTGACTCTGTAGGAGACC 1112

RESULT 6  
US-09-980-350-1  
; Sequence 1, Application US/09980350  
; GENERAL INFORMATION:  
; APPLICANT: HERVIEU, GUILLAUME JEAN  
; APPLICANT: MEADOWS, HELEN JANE  
; APPLICANT: RANDALL, ANDREW DAVID  
; TITLE OF INVENTION: USES OF H-TREK-1 POLYPEPTIDES AND  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: P32320  
; CURRENT APPLICATION NUMBER: US/09/980,350  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: PCT/GB00/02107  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: GB 9912733.4  
; PRIOR FILING DATE: 1999-06-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1246  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-980-350-1  
Alignment Scores:  
Pred. No.: 2,21e-193 Length: 1246  
Score: 1633.00 Matches: 356  
Percent Similarity: 98.91% Conservative: 8  
Best Local Similarity: 96.74% Mismatches: 4  
Query Match: 97.34% Indels: 0  
DB: 44 Gaps: 0

US-09-655-272-4 (1-370) x US-09-980-350-1 (1-1246)  
QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
DB 9 ATGCGGCACCTGACTTGGATCTTAAATCTGCGCTCAGAACTCCAAACCGAGGCTC 68  
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
DB 69 TCGTTTCCACGAAACCCACAGTCTTCTCCGGGTGGAGAGTGACACGCAATTAAT 128  
QY 41 ValMetLysThrLysThrValSerThrIlePhePheLeuValValValLeuThrLeuIle 60  
DB 129 GTTATGAAATGGAAGACGGTCTCCACGATATTCCTGGTGGTGTCTCTATCTGATCATC 188  
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80  
DB 189 GGAGCCACCGTGTTCAGAACCAATTCAGACGCTCATGAGATTCACAGAGGACCAACCAT 248  
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 249 GTGATCCAGAGCAACCAATTCATATCCCAATTCCTGTGTCTCAATTCGACGGAGCTGGAT 308  
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
DB 309 GAACCTCATTCAGCAAAATAGTGGCAGCAATAAATGAGGAGATTATACCGTTAGGAAACACC 368  
QY 121 SerAsnGlnValSerHisThrAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 369 TCCATCAATCAGTCACTCTGGATTTGGGAAGTTCTTCTTCTTGTGGCACTGTATT 428  
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysIle 160  
DB 429 ACAACCATAGGATTTGGAAACATCTCACACGACAGAAAGCGGCAAAATATTCGTATC 488  
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
DB 489 ATCTATGCTTACTGGGAATTCCTCTCTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG 548  
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysThrAsn 200  
DB 549 CTAGGCACCAATTTGGAAAGGAATTCCAAGTGGAAAGATACGTTTATTAAAGTGAAT 608  
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
DB 609 GTTAGTCAGACCAAGATTGGCATCATCTCAACAATCATATTTATATCTTTGGCTGTGTA 668  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyThrSerAlaLeuAsp 240  
DB 669 CTCCTTTGGCTCTGGCTGGATCATATTCACAACATAGAGGCTGGAGTGCCTGGAC 728  
QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
DB 729 GCCATTTATTTTGGTTATCACTCTCAACAATTCATTTGGATTTGGTACCTTGCAGGT 788  
QY 261 GlySerAspLeuGluThrLeuAspPheTyrLysProValValThrPheThrIleLeuVal 280  
DB 789 GGATCCGATATTGAATATCTGGACTCTATAGCCTGTCTGTGGTCTGGATCTTGTGA 848  
QY 281 GlyLeuAlaThrPheAlaAlaValLeuSerMetIleGlyAspThrLeuArgValIleSer 300  
DB 849 GGGCTTGCCTTACTTCTGCTGCTGAGCATGATTGGAGATTTGGCTCCGAGTGATATCT 908  
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluThrAlaAsn 320  
DB 909 AAAAAGACAAAGAGAGTGGAGAGTTCCAGAGCACACGCTGCTGAGTGGACAGCAAC 968  
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluLeuLeuThrAspLysPhe 340  
DB 969 GTACAGCCGAATTCNAAGAAACAGAGGCGAGTGGAGTGGAGATTATGACAAAGTTC 1028  
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360

Db 1029 CAGCGGCGACCTCCATCAAGCGGAAGCTCTCGGAGAACTGCTGGAAACCAATCAG 1088  
Qy 361 GluLeuThrProCysMetArgThr 368  
Db 1089 GAGCTGACTCCTTGTAGGAGGACC 1112  
RESULT 7  
US-10-036-657-35  
; Sequence 35, Application US/10036657  
; GENERAL INFORMATION:  
; APPLICANT: Earl Francis Albone, et al.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES  
; FILE REFERENCE: GP-707788-CL  
; CURRENT FILING DATE: US/10/036, 657  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; LENGTH: 1246  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-10-036-657-35  
Alignment Scores:  
Pred. No.: 2,21e-193 Length: 1246  
Score: 1833.00 Matches: 356  
Percent Similarity: 98.91% Conservative: 4  
Best Local Similarity: 96.74% Mismatches: 0  
Query Match: 97.34% Indels: 0  
DB: 45 Gaps: 0  
US-09-655-272-4 (1-370) x US-10-036-657-35 (1-1246)  
Qy 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
Db 9 ATGGCGGACCTGACTTGTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC 68  
Qy 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
Db 69 TCGTTTCCAGAAACCCACAGTGTCTTCCCGGTGGAGAGTGACACGACCAATTAAT 128  
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuThrLeuIle 60  
Db 129 GTTATGAATGGGAAGACGGTCTCCAGATATCTCGTGGTGTCTCTATCTGATCATC 188  
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrile 80  
Db 189 GGAGCCACCGTGTTCAGACATTTGGAGCAGCCTCATGAGATTTTCAGAGGACCACTT 248  
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
Db 249 GTGATCCAGAAGCAAAACATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 308  
Qy 101 GluLeuIleGlnGlnLeuValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
Db 309 GAATCATTCAGCAAAATAGTGGCAGCAATAAATGCGAGGATTTATACCGTTAGGAACACC 368  
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
Db 369 TCCAAATCAATAGTCACTGGGATTTGGGAAGTCTCTTCTTGTGCACTGTAT 428  
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
Db 429 ACAACCATAGATTTGGAACATCTCCACGACGACAGAGCGGCAAAATATTCGTATC 488  
Qy 161 IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
Db 489 ATCTATGCTCTTACTGGGAATTCCTCTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG 548  
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
Db 549 CTAGGCGACCATATTTGGAAAGAAATGGCCAAAGTGGAGATACGTTTATTAAGTGAAT 608

Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
Db 609 GTTAGTCAGACCAAGATTCGCATCATCTCAACAATCATATTTATATCTTTGGCTGTGA 668  
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
Db 669 CTCCTTGTGGCTCTGCTGCGATCATATTCAAACACATAGAGGCTGGAGTGGCCCTGGAC 728  
Qy 241 AlaIleTyPheValValIleThrLeuThrIleGlyPheGlyAspTyValAlaGly 260  
Db 729 GCCATTTATTTGTGGTTATCACTTAACAACATATTGGATTTGGTACTACGTTGCAGGT 788  
Qy 261 GlySerAspIleGluTyIleuAspPheTyLysProValValTrpPheTrpIleLeuVal 280  
Db 789 GGATCCGATATTGAATATCTGACTTCTATAAGCCCTGTCGTGGTCTCGGATCCTTGA 848  
Qy 281 GlyLeuAlaTyPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
Db 849 GGGCTTGTCTTACTTTGCTGCTGCTGACGATGATTTGGAGATTTGGCTCGAGTGATATCT 908  
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
Db 909 AAAAGACAAAGAGAGAGGCTGGAGAGTTTCAGAGCACACGCTGCTGAGTGGACAGCAAC 968  
Qy 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyAspLysPhe 340  
Db 969 GTACAGCCGAAATTCAAAGAAACCCAGAGGCGAGCTGAGTGTGGAGATTTATGCAAGTTC 1028  
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
Db 1029 CAGCGGCGCACCTCCATCAAGCGGAAGCTCTCGGCAAACTGCTGGAAACCAATCAG 1088  
Qy 361 GluLeuThrProCysMetArgThr 368  
Db 1089 GAGCTGACTCCTTGTAGGAGGACC 1112  
RESULT 8  
US-10-121-746-82  
; Sequence 82, Application US/10121746  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: Novel Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/10/121, 746  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: US/09/336,643A  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-08-07  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82  
; LENGTH: 3300  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (50) ... (1285)  
US-10-121-746-82  
Alignment Scores:  
Pred. No.: 8,31e-193 Length: 3300  
Score: 1833.00 Matches: 356  
Percent Similarity: 98.91% Conservative: 8  
Best Local Similarity: 96.74% Mismatches: 4

```
Query Match: 97.34% Indels: 0
DB: 47 Gaps: 0
US-09-655-272-4 (1-370) x US-10-121-746-82 (1-3300)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
DB 50 ATGGGGCACCTGACTGCTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC 109
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerSerAlaIleAsn 40
DB 110 TCGTTTTCCAGAAACCCAGAGTCTTCCCGGTGGAGAGTGCACAGCCATTAT 169
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60
DB 170 GTTATGAATGGAGAGAGTCTCCAGATATTCCTGGTGGTGTCTCTATCTGATCATC 229
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80
DB 230 GGAGCCACCGTGTTCAGAGCATTTGAGAGCAGCTCATGAGATTTTCAGAGGACCACT 289
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
DB 290 GTGATCCAGAAAGCAACATTCATATCCCAACATTCCTGTGTCAATTCGAGGAGCTGGAT 349
QY 101 GluLeuIleGlnIleValAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
DB 350 GAACATTCAGCAAAATAGTGGAGCAATTAATAGAGGATATATCCGTTAGGAACACC 409
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
DB 410 TCCAATCAATCAGTCAGTGGGATTTGGGAAGTTCCTTCTTCTTCTGCTGCACTGTATT 469

PCT-US99-03826-82
; Sequence 82, Application PC/TUS9903826A
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew
; APPLICANT: Curran, Mark
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15PCT
; CURRENT APPLICATION NUMBER: PCT/US99/03826A
; CURRENT FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,687
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: 60/095,836
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(1285)
PCT-US99-03826-82

Alignment Scores: 8,36e-193 Length: 3316
Pred. No.: 1833.00 Matches: 356
Score: 98.91% Conservative: 8
Percent Similarity: 96.74% Mismatches: 4
Best Local Similarity: 97.34% Indels: 0
Query Match: 1 Gaps: 0
DB: 1

US-09-655-272-4 (1-370) x PCT-US99-03826-82 (1-3316)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
DB 50 ATGGGGCACCTGACTGCTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC 109
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerSerAlaIleAsn 40
DB 110 TCGTTTTCCAGAAACCCAGAGTCTTCCCGGTGGAGAGTGCACAGCCATTAT 169
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60
DB 170 GTTATGAATGGAGAGAGTCTCCAGATATTCCTGGTGGTGTCTCTATCTGATCATC 229
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80
DB 230 GGAGCCACCGTGTTCAGAGCATTTGAGAGCAGCTCATGAGATTTTCAGAGGACCACT 289
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
DB 290 GTGATCCAGAAAGCAACATTCATATCCCAACATTCCTGTGTCAATTCGAGGAGCTGGAT 349
QY 101 GluLeuIleGlnIleValAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
DB 350 GAACATTCAGCAAAATAGTGGAGCAATTAATAGAGGATATATCCGTTAGGAACACC 409
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
DB 410 TCCAATCAATCAGTCAGTGGGATTTGGGAAGTTCCTTCTTCTTCTGCTGCACTGTATT 469
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QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysIle 160  
DB 470 ACAACCATAGGATTTGGAAACATCTCACACGACAGAGCGGCAAAATATTCTGTATC 529  
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
DB 530 ATCTATGCCCTTACTGGGAATTCCTCTTTGGTTTCTCTGGCTGGAGTTGGAGATCAG 589  
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleTyrAsn 200  
DB 590 CTAGGCACCATATTGGAAAGAAATTCACCAAGTGGAGATACGTTTATTAAAGTGGAA 649  
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
DB 650 GTTAGTCAGACCAAGATTCGATCATCTCAACATCATATTTATATATTGGCTGTGTA 709  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTyrSerAlaLeuAsp 240  
DB 710 CTCTTTGTGGCTCTGCTGCGATCATATTCAACACATAGAGCTGGAGTGCCTGGAC 769  
QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
DB 770 GCCATTATTCTGTGGTTATCACTCTAAACAATATTGGATTGGTGAATTCAGGT 829  
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
DB 830 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGTCTGTGGTTCTGGATCCTTGT 889  
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
DB 890 GGCTTGTCTTACTTGTCTGCTGCTGAGCATATTGGAGATTGGCTCCGAGTGATCT 949  
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
DB 950 AAAAGCAAAAGAGAGTGGGAGGTTCCAGAGCACGCTGCTGAGTGAGCAAGCAAC 1009  
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
DB 1010 GTCACAGCCGATTTCAAGAAACAGAGGCGACTGAGTGTGGAGATTTATGCAAGTTC 1069  
QY 341 GluArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
DB 1070 CAGCGGCGCACTTCATCAGCGGAGCTCTCGCAGAACTGGCTGGAACCAATCAG 1129  
QY 361 GluLeuThrProCysMetArgThr 368  
DB 1130 GAGCTGACTCTTGTAGGAGGACC 1153

## RESULT 10

US-10-170-235-27467  
; Sequence 27467, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
; FILE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF  
; FILE REFERENCE: CL001380  
; CURRENT APPLICATION NUMBER: US/10/170,235  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 42514  
; SEQ ID NO 27467  
; LENGTH: 3256  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-27467

## Alignment Scores:

Pred. No.:	2,28e-192	Length:	3256
Score:	1829.00	Matches:	355
Percent Similarity:	98.91%	Conservative:	9
Best Local Similarity:	96.47%	Mismatches:	4
Query Match:	97.13%	Indels:	0
DB:	48	Gaps:	0

US-09-655-272-4 (1-370) x US-10-170-235-27467 (1-3256)  
QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
DB 64 GTGGCGGACCTGACTTGTCTGGATCTCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 123  
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
DB 124 TCGTTTTCACGAAACCCACAGTGTCTTCCCGGTGGAGAGTGCACACGACCAATTAAT 183  
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIleIle 60  
DB 184 GTTATGAAATGGAGACGCTCTCCACATATCTCTGGTGTGTCTCTATCTGATCATC 243  
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
DB 244 GGAGCCACCGTGTTCAAAGCATTTGGAGACGCTCATGAGATTTTCACAGAGGACCACTT 303  
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 304 GTGATCCAGAAACCAATTCATATCCCAACATCTCTGTGTCAATTCGACGGAGCTGGAT 363  
QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
DB 364 GAACTCTTCGCAAAATAGTGGCAGCAATAATCGAGGATATACCGTTAGGAAACACC 423  
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 424 TCCAATCAAAATCAGTCACCTGGGATTTGGGAAGTCTCTCTCTTCTGGCTGGCACTGTATT 483  
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
DB 484 ACAACCATAGGATTTGGAAACATCTCACACGACAGAGCGGCAAAATATTCTGTATC 543  
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
DB 544 ATCTATGCTCTTACTGGGAATTCCTCTCTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG 603  
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleTyrAsn 200  
DB 604 CTAGGCACCATATTGGAAAGAAATTCGCAAGTGGAAAGATACGTTTATTAAAGTGGAA 663  
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
DB 664 GTTAGTCAGACCAAGATTCGATCATCTCAACAATCATATTTATATCTTGTGCTGTGTA 723  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
DB 724 CTCTTTGTGGCTCTGCTGCGATCATATTCAAAACATAGAGCTGGAGTGCCTGGAC 783  
QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
DB 784 GCCATTATTCTGTGGTTATCACTCTAAACAATTTGGATTTGGTCACTACGTTGCAGGT 843  
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
DB 844 GGATCCGATATTGAATATCTGCACTTCTATAAGCCTGTCTGTGGTTCTGGATCCTTGT 903  
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
DB 904 GGCTTGTCTTACTTGTCTGCTGCTGAGCATGATTTGGAGATTTGGCTCCGAGTGATATCT 963  
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
DB 964 AAAAGCAAAAGAGAGTGGGAGAGTTTCAGAGCACGCTGCTGAGTGAGCAAGCAAC 1023  
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
DB 1024 GTCACAGCGCAATTCAAAGAAACCCAGAGGCGACTGAGTGTGGAGATTTATGCAAGTTC 1083  
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
DB 1084 CAGCGGCGCACTCTCAATCAAGCGGAGGCTCTCGGCAAACTGGCTGGAAACCAATCAG 1143



QY 361 GluLeuThrProCysMetArgThr 368  
 Db 1144 GAGCTGACTCTTGTAGGAGGACC 1167

RESULT 11

US-60-443-566-876  
 ; Sequence 876, Application US/60443566  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001447  
 ; CURRENT APPLICATION NUMBER: US/60/443,566  
 ; CURRENT FILING DATE: 2003-01-30  
 ; NUMBER OF SEQ ID NOS: 25102  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 876  
 ; LENGTH: 3256  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-60-443-566-876

Alignment Scores:  
 Pred. No.: 2,28e-192 Length: 3256  
 Score: 1829.00 Matches: 355  
 Percent Similarity: 98.91% Conservative: 9  
 Best Local Similarity: 96.47% Mismatches: 4  
 Query Match: 97.13% Indels: 0  
 Gaps: 0

US-09-655-272-4 (1-370) x US-60-443-566-876 (1-3256)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 Db 64 GTGGCGGACCTGACTTGTGATCTTAAATCTCCGCTCAGAACTCCAAACCGAGGCTC 123  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 Db 124 TCGTTCCTCCAGAACCCACAGTGTCTTCCCGGTGGAGTGACAGCACTTAAT 183  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuThrIle 60  
 Db 184 GTTATGAATGGAGACGCTCTCCAGCATATCTCGTGGTGTCTCTATCTGATCATC 243  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluClnProGlnGluIleSerGlnArgThrIle 80  
 Db 244 GGAGCCACCGTGTTCAGAACCATTTGGAGCAGCTCATGAGATTTCCAGAGGACCACTT 303  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 Db 304 GTGATCCAGAGCAAAACATTCATATCCCAACATTCCTGTGTCAATTCAGCGAGCTGGAT 363  
 QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 Db 364 GAACCTCATTACGCAATAGTGGCAATAAATGCGGATATATACCTTTAGGAACACAC 423  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyValIle 140  
 Db 424 TCCAAATCAATCAGTCACTGGGATTTGGAAAGTTCCTTCTTCTTGTGGCAGCTGTTAT 483  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 Db 484 ACACCATAGGATTTGGAAACATCTCACACGACAGAGGGGCAAAATATTCGTATC 543  
 QY 161 IleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180  
 Db 544 ATCTATGCTTACTGGGAATTCCTCTTGTGTTTCTCTTGGCTGGAGTTGGAGATCAG 603  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 Db 604 CTAGGCACCATATTTGGAAAGGAATTTGCCAAAGTGGAGATACGTTTATTAAGTGGAT 663

QY 201 ValSerGlnThrLysIleArgIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 Db 664 GTTAGTCAGACCAAGATTGCGATCATCTCAACATCATATTTATATATTTGGCTGTGTA 723  
 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 Db 724 CTCTTTGTGGCTCTGCGCTGCGATCATATTTCAACACATAGAGCTGGAGTCCCTGGAC 783  
 QY 241 AlaIleTrpPheValValIleThrLeuThrThrIleGlyPheGlyAspTrpValAlaGly 260  
 Db 784 GCCATTTATTTGGTGTATCACTCTCAACATATTTGGAATTTGGTGTGACTACGTTGCAGGT 843  
 QY 261 GlySerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleVal 280  
 Db 844 GGATCCGATATTTGAATATCTGCACTTCTATTAAGGCTGTCTGTGTCTGTGATCCTGTGA 903  
 QY 281 GlyLeuAlaTrpPheAlaValLeuSerMetIleGlyAspTrpLeuAlaGlyValIleSer 300  
 Db 904 GGGCTTGTCTTACTTTGCTGCTGCTGAGCATGATTTGGAGATTTGGCTCCGAGTGTATCT 963  
 QY 301 LysLysThrLysGluGluValClyGluPheArgAlaHisAlaGluTrpThrAlaAsn 320  
 Db 964 AAAAAGACAAAAGAGAGGTGGAGAGTTTCAGACACACGCTGTCTAGTGGACAGCAAC 1023  
 QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTrpAspLysPhe 340  
 Db 1024 GTACAGCGCAATTCAAAAGAAACCCAGGAGGCTGTAGTGGAGATTTATGCAAGTTC 1083  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisGln 360  
 Db 1084 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGAGAACTGGCTGGAAACCAACATCAG 1143  
 QY 361 GluLeuThrProCysMetArgThr 368  
 Db 1144 GAGCTGACTCTTGTAGGAGGACC 1167

RESULT 12

US-60-455-444-3496  
 ; Sequence 3496, Application US/60455444  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: BEGOVICH, Ann  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001455  
 ; CURRENT APPLICATION NUMBER: US/60/455,444  
 ; CURRENT FILING DATE: 2003-03-18  
 ; NUMBER OF SEQ ID NOS: 50986  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3496  
 ; LENGTH: 3256  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-60-455-444-3496

Alignment Scores:  
 Pred. No.: 2,28e-192 Length: 3256  
 Score: 1829.00 Matches: 355  
 Percent Similarity: 98.91% Conservative: 9  
 Best Local Similarity: 96.47% Mismatches: 4  
 Query Match: 97.13% Indels: 0  
 Gaps: 0

US-09-655-272-4 (1-370) x US-60-455-444-3496 (1-3256)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 Db 64 GTGGCGGACCTGACTTGTGATCTTAAATCTCCGCTCAGAACTCCAAACCGAGGCTC 123  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 Db 124 TCGTTCCTCCAGAACCCACAGTGTCTTCCCGGTGGAGATGACAGCACTTAAT 183

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Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrLeuIle 60
Db 184 GTTATGAAATGGAGAGCGTCTCCACGATATCTCTGGTGTCTCTCTATCTGATCATC 243
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnIleSerGlnArgThrIle 80
Db 244 GGAGCCACCGTGTCAAGCATTTGGAGCAGCCTCATGAGATTTACAGAGGACACCAT 303
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 304 GTGATCCAGAACCAACATTCATCCCAATCTCTGTCTCAATTCGACGGAGCTGGAT 363
Qy 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 364 GAATCATTCAGCAATAGTGGAGCAGCAATAATGACGGATATATCCGTTAGGAACACC 423
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerPhePheAlaGlyThrValIle 140
Db 424 TCCAAATCAAATCAGTCACCTGGGATTTGGGAAGTTCTCTCTCTCTGCTGGACTGTATT 483
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160
Db 484 ACAACCATAGGATTTGGAAACATCTCCACCGCAGCAATTAATGAGGATATATCCGTTAGGAACACC 543
Qy 161 IleTyrAlaLeuLeuGlyIleIlePheLysAlaGlyIleIleProLeuGlyAsnSer 180
Db 544 ATCTATGCCCTTACTGGGAATTCCTCTTGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 603
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 604 CTAGGCACCATATTTGGAAAGGAATTTGCCAAGTGGGAAGTTCCTCTCTCTCTCTCTCT 663
Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 664 GTTAGTCAGACCAAGATTCGATCACTCAACCAATCATATTTATATCTATTTGGCTGTGTA 723
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 724 CTCTTTGTGGCTCTGCTCGCATCATATTCAAACACATAGAGGCTGGAGTGCCTGGAC 783
Qy 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 784 GCATTTATTTTGTGGTATATCTCTCTCAACCAATCATATTTATATCTATTTGGCTGTGTA 843
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 844 GGATCCGATATTGATATCTGGACTTCTATAGCCTGTCTGTGGTCTCTGGATCCTTGTA 903
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 904 GGGCTTGCTTACTTTGCTGCTGCTGAGCATGATTTGGAGATTTGGCTCGGAGTGATATCT 963
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 964 AAAAAGCAAAAGAGAGGTGGAGAGTTCCAGAGCACACGCTCTCTGAGTGGACAGGCAAC 1023
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 1024 GTACAGCCGATTTCAAGAAACACAGGAGGCGACTGAGTGGAGATTTATGACAAGTTTC 1083
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1084 CAGCGGCCACCTCCATCAAGCGAGAGCTCTCGCGAAGCTGCTGGAAACCAACATCAG 1143
Qy 361 GluLeuThrProCysMetArgThr 368
Db 1144 GAGCTGACTCTCTGTAGGAGGACC 1167
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RESULT 13

US-60-465-241-3496

; Sequence 3496, Application US/60465241

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: BEGOVICH, Ann

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001468

; CURRENT APPLICATION NUMBER: US/60/465, 241

; CURRENT FILING DATE: 2003-04-23

; NUMBER OF SEQ ID NOS: 258418

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3496

; LENGTH: 3256

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-60-465-241-3496

Alignment Scores:

Pred. No.:	2,28e-192	Length:	3256
Score:	1829.00	Matches:	355
Percent Similarity:	98.91%	Conservative:	9
Best Local Similarity:	96.47%	Mismatches:	4
Query Match:	97.13%	Indels:	0
DB:	112	Gaps:	0

US-09-655-272-4 (1-370) x US-60-465-241-3496 (1-3256)

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Qy 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 64 GTGGCGGCACCTGACTTGTGGATCCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 123
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Qy 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 124 TCGTTTTCACGAAACCCACAGTGTCTTCCCGGTGGAGAGTGCACACGACCACTTAAT 183
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Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrLeuIleIle 60
Db 184 GTTATGAAATGGAGACGCTCTCCAGATATTTCTGGTGTGTCTCTCTATCTGATCATC 243
```

```
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80
Db 244 GGAGCCACCGTGTTCAAAGCATTTGGAGCAGCCTCATGAGATTTTCAGAGGACCACTT 303
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```
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 304 GTGATCCAGAACCAACATTCATATCCCAACATTTCTGTGTCAATTCGACGGAGCTGGAT 363
```

```
Qy 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 364 GAATCATTCAGCAATATAGTGGAGCAATTAATGAGGATATATCCGTTAGGAACACC 423
```

```
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 424 TCCAAATCAAATCAGTCACCTGGGATTTGGGAAGTTCTCTCTCTCTGCTGGACTGTATT 483
```

```
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160
Db 484 ACAACCATAGGATTTGGAAACATCTCCACCGCAGCAATTAATGAGGATATATCCGTTAGGAACACC 543
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```
Qy 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 544 ATCTATGCCCTTACTGGGAATTTCCCTCTTTGGTCTCTCTGCTGGAGTTGGAGATCAG 603
```

```
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 604 CTAGGCACCATATTTGGAAAGGAATTTGCCAAGTGGAAAGATACGTTTATTAAGTGGAAAT 663
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```
Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 664 GTTAGTCAGACCAAGATTCGATCATCTCAACAATCATATTTATATCTATTTGGCTGTGTA 723
```

```
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 724 CTCTTTGTGGCTCTGCTCGCATCATATTCAAACACATAGAGGCTGGAGTGCCTTGAC 783
```

```
QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 784 GCCATTTATTTGGTTATCACTCAACAACTATTGGATTGGTACACTACGTTGAGGT 843
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 844 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGTCTGTGGTTCTGGATCCTTGA 903
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 904 GGGCTTGTCTTACTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 963
QY 301 LysIleThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTyrTrpAlaAsn 320
Db 964 AAAAAGCAAAAGAGAGGTGGAGAGTTCCAGAGCACACGCTGCTGAGTGGACAGCCAC 1023
QY 321 ValThrAlaGluPheLysGluThrArgArgLysSerValGluIleTyrAspLysPhe 340
Db 1024 GTCACAGCCGAATTCAAAGAAACCCAGGAGCGACTGAGTGTGGAGATTTATGACAAAGTTC 1083
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1084 CAGCGGCCACCTCCATCAACGGAAGCTCTCGGCAAGCTGCTGGAAACCAATCAG 1143
QY 361 GluLeuThrProCysMetArgThr 368
Db 1144 GAGCTGACTCTTGTAGGAGACC 1167

RESULT 14
PCT-US03-01911-9
; Sequence 9, Application PC/TUS0301911
; GENERAL INFORMATION:
; APPLICANT: RAMANATHAN, Chandra
; APPLICANT: GOPAL, Shuba
; APPLICANT: MINTIER, Gabe
; APPLICANT: FEDER, John
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: D0210 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/01911
; CURRENT FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 9
; LENGTH: 2391
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
PCT-US03-01911-9

Alignment Scores:
Pred. No.: 2,5e-192 Length: 2391
Score: 1827.00 Matches: 354
Percent Similarity: 98.91% Conservatives: 10
Best Local Similarity: 96.20% Mismatches: 4
Query Match: 97.03% Indels: 0
DB: 2 Gaps: 0

US-09-655-272-4 (1-370) x PCT-US03-01911-9 (1-2391)
QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 586 TTGGCGGCACCTGACTTGTGGTAAATCTGCGCTCAGAACTCCAAACCCGAGGCTC 645
QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 646 TCGTTTTCCAGAAACCCACAGTGTCTTCCCGGGTGGAGTGACACCACTTAAT 705
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60
Db 706 GTTATGAATGAAGACGGTCTCCACGATATTCCTGGTGTGTCTTCTATCTATCATC 765
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80
```

```
Db 766 GGAGCCACCGTGTTCAAAGCATTTGGAGCAGCCTCATAGATTTTCAGAGGACCACTT 825
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 826 GTGATCCAGAACCAACATTCATATCCCAACATTCCTGTGTCAATTCGACGAGCTGGAT 885
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 886 GAACCTCATTCAGCAATAGTGGCAGCAATTAATGAGGAGTATATACCGTTAGGAACACC 945
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 946 TCCAAATCAATCAGTCACTGGGATTTGGAAAGTTCCTTCTTCTTCTTCTTCTTCTTCT 1005
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160
Db 1006 ACAACCATAGGATTTGGAAACATCTCACACGACAGAGCGGCAAAATATTCGTATC 1065
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 1066 ATCTATGCTTACTGGGAATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1125
QY 181 LeuGlyThrIlePheGlyGlyGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 1126 CTAGGCACCATATTTGGAAAGGAATTCGCAAGTGGAGATACGTTTATTAAGTGAAT 1185
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 1186 GTTAGTCAGACCAAGATTCGCATCATCTCAACAATCATATTTATATCTTCTTCTTCT 1245
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 1246 CTCTTTGTGCTCTGCTCGCATCATTTCAAAACACATAGAAAGGCTGGAGTCCCTGGAC 1305
QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 1306 GCATTTATTTTGTGTGTATCACTTCAACACTATTGGATTGGTACCTACGTTGAGGT 1365
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 1366 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGTCTGTGTCTTCTGGATCCTTGA 1425
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 1426 GGGCTTGTCTTACTTGTCTGCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 1485
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 1486 AAAAGCAAAAGAGAGGTGGAGAGTTCAAGACACACGCTGCTGAGTGGACGCAAC 1545
QY 321 ValThrAlaGluPheLysGluThrArgArgLysSerValGluIleTyrAspLysPhe 340
Db 1546 GTCACAGCCGAATTCAAAGAAACCCAGGAGCGACTGAGTGTGGAGATTTATGACAAAGTTC 1605
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1606 CAGCGGCCACCTCCATCAAGCGGAAGCTCTCGGCAAGCTGCTGGAAACCAATCAG 1665
QY 361 GluLeuThrProCysMetArgThr 368
Db 1666 GAGCTGACTCTTGTAGGAGACC 1689
```

## RESULT 15

US-10-349-528-9

; Sequence 9, Application US/10349528

; GENERAL INFORMATION:

; APPLICANT: RAMANATHAN, Chandra

; APPLICANT: GOPAL, Shuba

; APPLICANT: MINTIER, Gabe

; APPLICANT: FEDER, John

; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF

; TITLE OF INVENTION: USE THEREOF

; FILE REFERENCE: D0210

;; CURRENT APPLICATION NUMBER: US/10/349,528  
;; CURRENT FILING DATE: 2003-01-22  
;; NUMBER OF SEQ ID NOS: 35  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 9  
;; LENGTH: 2391  
;; TYPE: DNA  
;; ORGANISM: HOMO SAPIENS  
US-10-349-528-9

Alignment Scores:  
Pred. No.: 2,5e-192 Length: 2391  
Score: 1827.00 Matches: 354  
Percent Similarity: 98.91% Conservative: 10  
Best Local Similarity: 96.20% Mismatches: 4  
Query Match: 97.03% Indels: 0  
DB: 51 Gaps: 0

US-09-655-272-4 (1-370) x US-10-349-528-9 (1-2391)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
DB 586 TTGGCGGCACCTGACTTGTGGATCTAAATCTCCGCTCAGAACTCCAAACCGAGGCTC 645  
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
DB 646 TCGTTTTCACGAAACCCACGAGTGTCTTCCCGGTGGAGGTGACACGACCACTAAT 705  
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60  
DB 706 GTTATGAATGGAGACGGTCTCCAGATATCTCGGTGGTGTCTCTATCTGATCATC 765  
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnIleSerGlnArgThrIle 80  
DB 766 GGAGCCACCGTGTCAAGCATTTGGAGAGCGCTCATGAGATTTCAAGAGGACCACTT 825  
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 826 GTGATCCAGAACCAACATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 885  
QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
DB 886 GAATCATTCAGCAATATAGTGGAGCAATATATGAGGATATATACCGTTAGGAACACC 945  
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 946 TCCATCAATCAGTCACTGGGATTTGGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1005  
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
DB 1006 ACAACCATAGGATTTGGAAACATCTCACACGACAGAGGCGGCAAAATATTTCTGTATC 1065  
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180  
DB 1066 ATCTATGSCCTTACTGGGAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1125  
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
DB 1126 CTAGGCACCATATTTGGAAAGGAATGCCAAGTGGAGATACGTTTATTAAGTGAAT 1185  
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
DB 1186 GTTAGTCAGACCAAGATTCGATCATCTCAACAATCATATTTATATATTTTGGCTGTGTA 1245  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
DB 1246 CTCCTTTGTGGCTCTGCGCTCGATCATATTAACAACATAGAGGCTGGAGTGCCTGGAC 1305  
QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
DB 1306 GCCATTTATTTGTGGTTATCACTCTACAACTATTTGGATTTGGTGTGACTACGTTGAGGT 1365  
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280

Search completed: February 3, 2005, 06:23:45  
Job time : 4488.83 secs

DB 1366 GGATCGATATTGAATATCTGGACTTCTATAAGCCTGTGTGTGGTCTTGGATCCTTGA 1425  
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
DB 1426 GGGCTTGTCTTACTTGTCTGTCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 1485  
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
DB 1486 AAAAAGACAAAAGAGAGGTGGAGAGTTCAAAGCACACGCTGCTGAGTGGACAGCAAC 1545  
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
DB 1546 GTACACAGCCGATTTCAAGAAACCGAGGCGACTGAGTGTGGAGATTTATGACAAGTTC 1605  
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
DB 1606 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGAGAACTGCTGGAAACCAACATCAG 1665  
QY 361 GluLeuThrProCysMetArgThr 368  
DB 1666 GAGCTGACTCCTTTGAGGAGGACC 1689

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 21:56:31 ; Search time 3769.86 Seconds  
(without alignments)  
3576.449 Million cell updates/sec

Title: US-09-655-272-4  
Perfect score: 1883  
Sequence: 1 MAAPDLLDPKSAQNSKPRL.....SALAGNHQELTPCMTCL 370

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DBV=xlh  
-O=/cgn2\_1/USPTO.spool.US09655272/runat\_02022005\_141715\_6758/app.query.fasta\_1.1102  
-DB=EST -QPM=fastap -SUFFIX=est -MINMATCH=0.1 -LOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09655272 @CGN 1 1 4385 @runat\_02022005\_141715\_6758 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*	Query	Match	Length	ID	Description
1: gb_est1:*	1663	88.3	1113	9	AY418067 Mus muscu
2: gb_est2:*	1646	87.4	1113	9	AY418065 Homo sapi
3: gb_htc:*	1252.5	66.5	1745	3	AK036066 Mus muscu
4: gb_est3:*	1252.5	66.5	2534	3	AK082153 Mus muscu
5: gb_est4:*	1225.5	65.1	2628	3	AK031904 Mus muscu
6: gb_est5:*	1211	64.3	1113	9	AY418066 Pan trogl
7: gb_est6:*	1134	60.2	713	6	CB526721 UT-M-PYO
8: gb_gsa1:*	1106	58.5	920	5	BQ948206 AGENCOURT
9: gb_gsa2:*	1045	55.5	654	7	CK005597 AGENCOURT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1663	88.3	1113	9	AY418067 Mus muscu
2	1646	87.4	1113	9	AY418065 Homo sapi
3	1252.5	66.5	1745	3	AK036066 Mus muscu
4	1252.5	66.5	2534	3	AK082153 Mus muscu
5	1225.5	65.1	2628	3	AK031904 Mus muscu
6	1211	64.3	1113	9	AY418066 Pan trogl
7	1134	60.2	713	6	CB526721 UT-M-PYO
8	1106	58.5	920	5	BQ948206 AGENCOURT
9	1045	55.5	654	7	CK005597 AGENCOURT

10	955	50.7	834	7	CO248930	AGENCOURT
11	949	50.4	827	7	CO249404	AGENCOURT
12	945.5	50.2	840	7	CO247814	AGENCOURT
13	943	50.1	760	5	BU610944	UT-M-FCO-
14	932.5	49.5	854	7	CO249306	AGENCOURT
15	929	49.3	832	7	CO245300	AGENCOURT
16	924.5	49.1	598	6	CF171014	AGENCOURT
17	912	48.4	537	5	BX478651	DKF2p866H
18	911	48.4	775	7	CN528767	UT-M-HQO-
19	876	46.5	784	5	BQ042251	UT-M-BQO-
20	862	45.8	869	5	BU956092	AGENCOURT
21	817	43.4	479	6	CA871490	K0910F08-
22	797	42.3	1182	9	AY405804	Homo sapi
23	793	42.1	532	6	CD625302	55013674J
24	793	42.1	532	6	CD625313	55013751H
25	793	42.1	532	6	CD625322	55013895J
26	793	42.1	533	6	CD625314	55013751J
27	790	42.0	532	6	CD625321	55013895H
28	787	41.8	653	6	CD625233	55013078H
29	784	41.6	473	6	CA890051	B0156604-
30	778	41.3	528	6	CD625319	55013886H
31	778	41.3	529	6	CD625318	55013878J
32	778	41.3	532	6	CD625304	55013675J
33	777	41.3	530	6	CD625320	55013886J
34	776	41.2	533	6	CD625301	55013674H
35	775	41.2	533	6	CD625310	55013727J
36	775	41.2	544	6	CD625324	5501620J
37	775	41.2	592	6	CD625296	55013079J
38	775	41.2	631	6	CD625292	55013076J
39	772	41.0	577	6	CD625330	55041676J
40	770.5	40.9	1197	9	AY405806	Mus muscu
41	767	40.7	531	6	CD625308	55013711J
42	767	40.7	535	6	CD625300	55013626J
43	766	40.7	487	6	CD625298	55013183J
44	765	40.6	530	6	CD625317	55013878H
45	759	40.3	531	6	CD625312	55013735J

# ALIGNMENTS

RESULT 1	AY418067	1113 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY418067	Mus musculus KMK2 gene, VIRTUAL TRANSCRIPT, partial sequence,			
DEFINITION	AY418067	Genomic survey sequence.			
ACCESSION	AY418067.1	GI:39774027			
VERSION	GSS.				
KEYWORDS	Mus musculus (house mouse)				
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 1113)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1113)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment				
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US-09-655-272-4 (1-370) x AY418067 (1-1113)

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US-09-655-272-4 (1-370) x AY418065 (1-1113)

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QY 82 IleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAspGlu 101
DB 121 ATCCAGAAGCAGACCTTCATAGCCAGCATGCCCTGGCTCAACTCCACCGAGCTGGACGAA 180
QY 102 LeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSerSer 121
DB 181 CTATCCAGCAATATAGTGGCAGCATATACGAGGATTTATCCCTTAGGAACAGCTCC 240
QY 122 AsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIleThr 141
DB 241 AATCAAGTTAGTCACTGGACCTCGGAAGCTCTTCTTCTTCTTGTGTACTGTATCACA 300
QY 142 ThrIleGlyPheGlyAsnIleSerProArgThrGluGlyIlePheCysIleIle 161
DB 301 ACCATAGATTGGAAACATCTCCCCAGCACTGAAGTGGAAATATTTCTGCAATC 360
QY 162 TyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGlnLeu 181
DB 361 TATGCTTGTGGGAATTCCTCTTGGCTTCTTCTGCTGGGTGGTGTGATCAGCTA 420
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DB 421 GGAACTATATTGGAAAAGGAATTCGCCAAAGTGGAAAGACACATTTATTAAGTGGAAATGTT 480
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DB 541 TTTGTGGTCTCCCTCGGTCTATATCAAGCACATAGAGGCTGGAGCGCCTGGAGCCT 600
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DB 601 ATCTATTGTGGTTATCACTCTGACGACCATTTGGATTGGAGACTACGTGGCAGGTGGA 660
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DB 721 CTGGCCTACTTTCAGCTGTTCTGAGCATGATTGGGGACTGGCTACGGGTGATCTCTAAG 780
QY 302 LysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTyrTrpAlaAsnVal 321
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ORIGIN
Alignment Scores:
Pred. No.: 1,21e-142 Length: 1745
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Best Local Similarity: 65.52% Mismatches: 66
Query Match: 66.52% Indels: 11
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US-09-655-272-4 (1-370) x AK036066 (1-1745)

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QY 38 --AlaIleAsnValMetLysTrpLysThrValSerThrIlePheLeuValValLeu 56
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QY 57 TyrLeuIleIleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGln 76
DB 621 TACCTCTCACTGGTGGCTTGTCTTCGGGCTTGGAAACAGCCCTTCGAGAGCAGTCAG 680

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/tissue type="cerebellum"
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/dev_stage="16 days neonate"
387. >1745
/notes="unnamed protein product; POTASSIUM CHANNEL
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CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT)
homolog [Rattus norvegicus] (SWISSPROT|Q9JIS4, evidence:
FASTA, 99.4%ID, 97.2%length, match=1569)
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GDFVAGNAGINRYKWKPLVFMILVGLAYFAAVALSMIGDMLRVLSKTKKEVGEIK
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TK3"

ORIGIN
Alignment Scores:
Pred. No.: 1,21e-142 Length: 1745
Score: 1252.50 Matches: 247
Percent Similarity: 79.58% Conservative: 53
Best Local Similarity: 65.52% Mismatches: 66
Query Match: 66.52% Indels: 11
DB: 3 Gaps: 5

US-09-655-272-4 (1-370) x AK036066 (1-1745)

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DB 444 GCAGCCACCAGGTGTCAGCCAGCCAGAGTGCCACTAACGGGCATCACCCCTGTCTCTCGA 503

QY 20 LeuSerPheSerLysProThrValLeuAlaSerArgValGluSerAspSer----- 37
DB 504 CTCTCCATTTCTCTCAGCAGCCAGGTGTAGCC---AGGATGAAGCGCGCTCCAGGGA 560

QY 38 --AlaIleAsnValMetLysTrpLysThrValSerThrIlePheLeuValValLeu 56
DB 561 GGCTCGCAACAGTATTGAAGTGAACAGAGTGTCCTCCATCTCTGTTGGTGGTGGTC 620

QY 57 TyrLeuIleIleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGln 76
DB 621 TACCTCTCACTGGTGGCTTGTCTTCGGGCTTGGAAACAGCCCTTCGAGAGCAGTCAG 680

QY 77 ArgThrThrIleValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSer 96
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QY 97 ThrGluLeuAspGluIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIlePro 116
DB 741 CAGGAACATAGACACATGATTCAGATCGATCGATCGATGATACCGCGGAGTCAGCCCA 800

QY 117 LeuGlyAsnSerSerAsnGlnValSerHieTrpAspLeuGlySerSerPhePheAla 136
DB 801 GTAGAAACTCTTCCACAGCAGCAGTCACTGGGACCTTGGAAAGTGCCTTCTCTTTGCT 860

QY 137 GlyThrValIleThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLys 156
DB 861 GGGACAGTCATCAACACATAGGTATGGGAATATTCCTCGAGCACTGAAGGAGGCAAA 920

QY 157 IlePheCysIleIleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGly 176
DB 921 ATCTTTGTATTTTATATGCACTTTTGGGATCCCGCTTTTGGTTCTTATTGCTGGA 980

177 ValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPhe 196
981 ATTGGAGACCAACTTGGAAACCATCTTTGGCAAAAGCATTCGCAAGAGTGGAAGGTTTTT 1040

197 IleLysTrpAsnValSerGlnThrIleValIleArgIleIleSerThrIleIlePheIleLeu 216
1041 CGAAAGAACCAAGTGGAGCCAGCAAGATCCGGGTCATCTCCACGATCTCTTCACTTGG 1100

217 PheGlyCysValLeuPheValAlaAlaValIlePheLysHisIleGluGlyTrp 236
1101 GCTGGCTGATCGTGTGTGTGACCATCCCTGCTGTCATCTTTAAATACATCAGGAGTTGG 1160

237 SerAlaLeuAspAlaIleTrpPheValValIleThrLeuThrIleGlyPheGlyAsp 256
1161 ACCGCTTGGAGTCCATCTACTTTGTGTAGTACCGCTGACCAACAGTCTTGGTGTAT 1220

257 TyrValAlaGlyGly---SerAspIleGluTrpLeuAspPheTrpLysProValValTrp 275
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276 PheTrpIleLeuValGlyLeuAlaTrpPheAlaAlaValLeuSerMetIleGlyAspTrp 295
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316 GluTrpThrAlaAsnValThrAlaGluPheLysGluThrArgArgLeuSerValGlu 335
1401 GAGTGAAGCGCTAAATGTCTACTGCTGAGTTCCGGGAGACGAGAGCGGCTCAGCGTTGAG 1460

336 IleTyAspLysPheGlnArgAlaThrSerVal-----LysArgLysLeuSer 351
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352 AlaGluLeuAlaGlyAsnHisGlnGluLeuThrProCysMetArgThr 368
1521 TTGGACAGAGCGGCCACTCACTGGACATGCTATCCCTGAGAACGCTTCT 1571

RESULT 4
AK082153 2534 bp mRNA linear HTC 03-APR-2004
LOCUS AK082153.1 GI:26349568
DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:C230015H11 product:POTASSIUM CHANNEL
SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN
TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog [Rattus norvegicus],
full insert sequence.
ACCESSION AK082153
VERSION AK082153.1 GI:26349568
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

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Qy	336	IleTyrrAspIlyPheGlnArgAlaThrSerVal-----LysArgIlyLeuSer	351
Db	1188	ATCATGACAGCTGTCACCGGAGCCACTATCCGAGTATGAGCGCGGAGCTGGGC	1247
Qy	352	AlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrProCysMetArgThr	368
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LOCUS	AK031904		
DEFINITION	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330442J09 product:POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog [Rattus norvegicus], full insert sequence.		
ACCESSION	AK031904		
VERSION	AK031904.1	GI:26082587	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253 10349636		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	2 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861		
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)		
REFERENCE	4 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation		
JOURNAL			
MEDLINE			
PUBMED			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
AUTHORS			

JOURNAL	of 60,770 full-length cDNAs		
REFERENCE	Nature 420, 563-573 (2002)		
AUTHORS	6 (bases 1 to 2628) Adachi, S., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, J., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Miyazaki, R., Miyazaki, A., Murata, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/		
FEATURES	Location/Qualifiers		
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Qy	20	LeuSerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSer-----	37
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Qy	38	---AlaIleAsnValMetLysTrpLysThrValSerThrIlePheLeuValValLeu	56
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QY 57 TyrllellelleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGln 76  
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 QY 97 ThrGluLeuAspGluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIlePro 116  
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 QY 117 LeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAla 136  
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 QY 237 SerAlaLeuAspAlaIleTyPheValValIleThrLeuThrIleGlyPheGlyAsp 256  
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 DEFINITION genomic survey sequence.  
 ACCESSION AY418066  
 VERSION AY418066.1 GI:39774026  
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 SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE 1 (bases 1 to 1113)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1113)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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 Best Local Similarity: 89.43% Mismatches: 23  
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 QY 62 AlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIleVal 81  
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 QY 142 ThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIleIle 161  
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SOURCE
ORGANISM      Mus musculus (house mouse)
REFERENCE
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/
TITLE        NIH-MGC
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M13879 row: c column: 09
High quality sequence start: 18
High quality sequence stop: 553.
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Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Average insert size 2.2 Kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."
ORIGIN
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Pred. No.: 5.16e-125 Length: 920
Score: 1106.00 Matches: 217
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Best Local Similarity: 99.09% Mismatches: 1
Query Match: 58.74% Indels: 1
DB: 5 Gaps: 0

US-09-655-272-4 (1-370) x BQ948206 (1-920)

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Qy 266 rLeuAspPheTyrIlySerProValValTyrPheTrpIleLeuValGlyLeuAlaTyrPheAl 286
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Qy 286 aAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSerLysIlyThrIlyGluG1 306
Db 425 AGCTGTCTTGAGCATGATTGGGACTGGCTACGGGTGATCTCTAAGAAGACGAAGGAAGA 484
Qy 306 uValGlyGluPheArgAlaHisAlaAlaGluTTrpThrAlaAsnValThrAlaGluPheLy 326
Db 485 GTTGGAGAGATTTCAGAGCGCATGCCCTGAGTGGACAGCCAAATGTACGGCCGAGTTCAA 544
Qy 326 sGluThrArgArgLeuSerValGluIleTyrAspLysPheGlnArgAlaThrSerVa 346
Db 545 GGAACGAGGAGGCGGCTGAGCTGAGATCTACGACAAAGTTCAGGCTCCACATCCGT 604
Qy 346 lLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrPro 364
Db 605 GAAGCGGAAACTCTCCGAGAGCTGGCGGCAAAACACACACAGCAACTGACTCCG 659

RESULT 9
LOCUS      CK005597          654 bp      mRNA      linear      EST 26-NOV-2003
DEFINITION AGENCOURT_16398134 NIH_MGC_229 Homo sapiens cDNA clone
IMAGE:30721772 5', mRNA sequence.
ACCESSION  CK005597
VERSION     CK005597.1 GI:38531639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 654)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgaaps-r@mail.nih.gov
            Tissue Procurement: Professor Miklas Palkovits
            cDNA Library Preparation: Michael Brownstein / Ted Usdin
            Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM270 row: f column: 21
            High quality sequence stop: 585.
FEATURES
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1. 654
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30721772"
/tissue_type="Human Brain - Frontal Cortex"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC 229"
/notes="Organ: brain/CNS; Vector: pDNR-LIB; Site 1: SfiI
(directional); Site 2: SfiI (directional); Library is
oligo-dT primed and directionally cloned.5' and 3'
adaptors were used in cloning as follows:
5'-AAGCATGGTATCAGCAGAGTGGCATTCAGCGCGG-3' 5'-ATTCTAGAGG
CCGAGCGCCGACATG-d(T)3N-IN-3. Full-length enriched
library was constructed using the Clontech Creator SMART
kit and size-selected for >0.5kb with an average insert
size of 1.2kb Library created in the laboratory of
Jonathan Kuo and Ted Usdin."
ORIGIN
Alignment Scores:
Pred. No.: 1.01e-117 Length: 654
Score: 1045.00 Matches: 208
Percent Similarity: 98.16% Conservative: 5
Best Local Similarity: 95.85% Mismatches: 4

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Query Match: 55.50% Indels: 1  
DB: 7 Gaps: 0

US-09-655-272-4 (1-370) x CK005597 (1-654)

QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuLeuIle 60  
DB 4 GTTATGAATGGAGAGCGGTCTCAGATATCTCTGGTGTCTCTATCTGATCATC 63

QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrThrIle 80  
DB 64 GGAGCCACCGTGTTCAAAGCATTTGGAGCAGCTCATGAGATTTACAGAGGACCACTT 123

QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 124 GTGATCCAGAGCAAAACATTCATATCCAACTTCTGTGTCAATTCGAGGAGCTGGAT 183

QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
DB 184 GAATCATTCAGCAATAGTGGCAGCAATTAATGAGGATATACCGTTAGGAACACC 243

QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 244 TCCAATCAATCAGTCACTGGGATTTGGGAAGTTCCTTCTTCTTGTGTCACCTGTATT 303

QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
DB 304 ACAACCATAGATTTGGAACATCTCCACGCGCAGAGGCGGCAAAATATTCGTATC 363

QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
DB 364 ATCTATGCTTACTGGGAATTCCTCTTGTGTTTCTTGTGCTGGAGTTGGAGATCAG 423

QY 181 LeuGlyThrIlePheGlyLysGlyAlaLysValGluAspThrPheIleLysTrpAsn 200  
DB 424 CTAGGCAACATATTGGAAAGGAATTCGCAAGTGGAGATGATTTATTAAAGTGAAT 483

QY 201 ValSerGlnThrLysIleAlaGlyIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
DB 484 GTTAGTCAGACCAAGATTCGATCATCTCAACATCATATTTATCTATTTGGCTGTGTA 543

QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
DB 544 CTCCTTTGGTCTGCTGCTGCGATCATATTCACACATAGAGGCTGGAGTGCCTGCAC 603

QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyr 257  
DB 604 GCCATTTATTTGTGGT-ATCACTCAACAACATTTGGATTTGTGACTAC 653

RESULT 10  
CO248930 LOCUS CO248930 834 bp mRNA linear EST 23-JUN-2004

DEFINITION AGENCOURT\_25900941 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:7286361 5', mRNA sequence.

ACCESSION CO248930  
VERSION CO248930.1 GI:49118782

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 834)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: IRB8 row: g column: 07  
High quality sequence start: 17  
High quality sequence stop: 670.  
Location/Qualifiers  
1. 834  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:7286361"  
/tissue\_type="mixed"  
/lab\_host="DHSA (T1 phage-resistant)"  
/clone\_lib="NIH MGC 195"  
/note="Vector: pDNR-Dual; Site 1: loxp-Sali; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/IRBX.preSV.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBX.preSV.dat)  
A Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 1,828-106 Length: 834  
Score: 955.00 Matches: 204  
Percent Similarity: 88.00% Conservative: 16  
Best Local Similarity: 81.60% Mismatches: 25  
Query Match: 50.72% Indels: 8  
DB: 7 Gaps: 2

US-09-655-272-4 (1-370) x CO248930 (1-834)

QY 1 MetalAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
DB 47 ATGGCGGACCTGACTTGTCTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC 106

QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
DB 107 TCGTTTTCACGAAACCCACAGTGTCTTCCCGGTGGAGAGTGACACGACCATTAAT 166

QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuLeuIle 60  
DB 167 GTTATGAATGGAGAGCGTCTCCAGATATCTCTGTGTGTCTCTATCTGATCATC 226

QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrThrIle 80  
DB 227 GGAGCCACCGTGTTCAAAGCATTTGGAGCAGCTCATGAGATTTACAGAGGACCACTT 286

QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 287 GTGATCCAGAGCAAAACATTCATATCCAACTTCTGTGTCAATTCGAGGAGCTGGAT 346

QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
DB 347 GAATCATTCAGCAATAGTGGCAGCAATAAATGAGGATATATACCGTTAGGAACACC 406

QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 407 TCCAATCAATCAGTCACTGGGATTTGGGAAGTTCCTTCTTCTTGTGTCACCTGTATT 466

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QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyValIlePheCysIle 160
D 467 ACAACCATAGGATTGGGAAACATCTCCACGACGACAGAGCGGCGCAAAATATTCGTGATC 526
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
D 527 ATCTATGCTTACTGGGAATCCCTCTTTGGTTTCTTCTTGGCTGGAGTTGAGATCAG 586
QY 181 LeuGlyThrIlePheGlyGlyValIleAlaLeuValGluAspThrPheIleLysTyrAsn 200
D 587 CTAGGCACCATATTTGGAAGGATT-GCCAAAGTGAAGATCG-TTATTAAGTGAAT 644
QY 201 ValSerGlnThrIleValIleArgIle-----IleSerThrIleIlePheIleLeuPheGly 218
D 645 GTTAGTCAGACCAAGAT-CGCACTCCCAACATCTATTAACTATTGCTGGTACCTGGGCC 703
QY 219 CysValLeuPhe-----ValAlaLeuProAlaValIlePheLysHisIleGluGly 235
D 704 TGTGCAATATCAACCTAAAGCTGATGCTGACCATTTATTTGTACCCACACATGATTGGA 763
QY 236 TrpSerAlaLeuAspAlaIleTyrPheVal 245
D 764 ACNTGGGATCATGAACGATATACGGGTC 793
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## RESULT 11

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CO249404
LOCUS CO249404
DEFINITION AGENCOURT 25900989 NIH MGC 195 Homo sapiens cDNA clone
IMAGE: 7286364 5', mRNA sequence.
ACCESSION CO249404
VERSION CO249404.1 GI:49120300
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 827)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRBK8 row: g column: 10
High quality sequence start: 15
High quality sequence stop: 639.
Location/Qualifiers
1..827
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7286364"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/note="Vector: pDNR-Dual; Site 1: loxP-Salt; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
```

## FEATURES

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source
1..827
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7286364"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/note="Vector: pDNR-Dual; Site 1: loxP-Salt; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
```

RESULT 12

of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [http://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](http://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat) a Note: this is a NIH\_MGC Library."

## ORIGIN

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Alignment Scores:
Pred. No.: 9,86e-106 Length: 827
Score: 949.00 Matches: 201
Percent Similarity: 85.43% Conservative: 16
Best Local Similarity: 79.13% Mismatches: 22
Query Match: 50.40% Indels: 17
DB: 7 Gaps: 3
US-09-655-272-4 (1-370) x CO249404 (1-827)
QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
D 46 ATGGCGGCACCTGACCTTGTGGATCCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 105
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
D 106 TCGTTTTTCACGAAACCCACAGTGTCTTCCGGGTGGAGAGTGACACGACCATTAAT 165
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60
D 166 GTTATGAAATGGAAGACGGTCTCCAGATATTCCTGGTGTCTCTATCTGATCATC 225
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80
D 226 GGAGCCACCGTGTTCAGACATTTGGAGCGCCTCATGAGATTTTCACAGAGACCACTT 285
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
D 286 GTGATCCAGAAAGCAAAACATTCATATCCCAACATTCCTGTGTCAATTCGACGAGCTGGAT 345
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
D 346 GAATCATTCAGCAATATAGTGGCAGCAATAATGCGAGGATTAATCCGTTAGGAACACC 405
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
D 406 TCCATCAATCAATCAGTCACCTGGGATTTGGGAGTTCCTTCTTCTTCTGCTGGCACTGTTAT 465
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160
D 466 ACAACCATAGGATTTGGAAACATCTCCACGACGACAGAAAGCGGCAAAATATTCGTGATC 525
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
D 526 ATCTATGCTTACTGGGAATCCCTCTTTGGTTTCTTCTTGGCTGGAGTTGAGATCAG 585
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLeuValGluAspThrPhe----- 196
D 586 CTAGGCACCATATTTGGAAGGATT-GCCAAAGTGAAGATCGTTTAAAGTGGATGTT 644
QY 197 IleLysTrpAsnValSerGlnThrIleValIleArgIleIleSerThrIleIlePheIleLeu 216
D 645 ATCAGACCAAAATTCCTCT-----CTCAACACTATTATCTATTG-CTG 685
QY 217 PheGlyCys-----ValLeuPheValAlaLeuProAlaValIlePheLys 231
D 686 GTACCTTGGCTGTGCTGCACTATCACATAAGCTGATGCTGAGCATTTATTTGTATCCA 745
QY 232 HisIleGluGlyTrpSerAlaLeuAspAlaIleTyrPheVal 245
D 746 CACATATGGACACTCGGTCAATGATCGACTCTACCGGTG 787
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CO247814  
LOCUS 840 bp mRNA linear EST 23-JUN-2004  
DEFINITION AGENCOURT 25900957 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:7286362 5', mRNA sequence.  
CO247814  
ACCESSION CO247814.1 GI:49114558  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-t@mail.nih.gov](mailto:cgabs-t@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: IRBK8 row: 9 column: 08  
High quality sequence start: 18  
High quality sequence stop: 627.  
Location/Qualifiers  
1. 840  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:7286362"  
/tissue\_type="mixed"  
/lab\_host="DH5A (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_195"  
/note="vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:  
loxP-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxP sites  
of the pDNR-dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)  
a Note: this is a NIH\_MGC library."

ORIGIN  
Alignment Scores:  
Pred. No.: 2,73e-105 Length: 840  
Score: 945.50 Matches: 198  
Percent Similarity: 86.69% Conservative: 17  
Best Local Similarity: 79.84% Mismatches: 26  
Query Match: 50.21% Indels: 8  
DB: 7 Gaps: 3

US-09-655-272-4 (1-370) x CO247814 (1-840)

Qy 1 MetalAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerIysProArgIeu 20  
Db 48 ATGGCGGCACTTGACTTGGATCCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 107  
Ov 21 SerPheSerIysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40

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FEATURES
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        /mol_type="mRNA"
        /strain="C57BL/6"
        /db_xref="taxon:10090"
        /clone="UI-M-FCO-cas-e-02-0-UI"
        /dev_stage="embryo 12.5 dpc"
        /tissue_type="whole brain"
        /lab_host="DH10B (TI phage resistant)"
        /clone_lib="NIH_BMAP_FCO"
        /notes="Organ: brain; vector: pyX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pyX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Alignment Scores:
Pred. No.: 4.75e-105 Length: 760
Score: 943.00 Matches: 190
Percent Similarity: 97.45% Conservative: 1
Best Local Similarity: 96.94% Mismatches: 5
Query Match: 50.08% Indels: 0
DB: 5 Gaps: 0

US-09-655-272-4 (1-370) x BU610944 (1-760)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAenSerLysProArgLeu 20
DB 172 GTGGGGCCCCCTGACTTGTCTGGATCCCAAGTCGTCTCAGAACTCCAAACCGAGGCTC 231
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
DB 232 TCATTCCTCTCAAAACCCACCGTGTCTTCCCGGTGGAGAGTGACTCGGCCATTAAT 291
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuThrIleIle 60
DB 292 GTTATGAAATGGGAAGACAGTCTCCACGATTTTCTGGTGTCTCTACCTGATCATC 351
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80
DB 352 GGAGCCACGGTGTTCAGGCGATTTGGAGCACCTTCAGGAGATTTCACAGAGACCACTT 411
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAenSerThrGluLeuAsp 100
DB 412 GTGATCCAGAAGCAGACACTTCATAGCCACGATGCTGCTCAACTCCACCGAGCTGGAC 471
QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAenSer 120
DB 472 GAACATCATCAGCAAAATAGTGGCAGCAATAAACGACGAGATTATCCCTTTAGGAAACAGC 531
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
DB 532 TCCAATCAAGTTAGTCTACCTGGACCTCGGAAGCTCTTCTCTTCTGTGTACTGTATC 591
QY 141 ThrThrIleGlyPheGlyAenIleSerProArgThrGluGlyGlyIlePheCysIle 160
DB 592 ACAACCATAGGATTTGGAAACATCTCCCCACGAACTGAAGGTGGAAAAATATTCGTCATC 651
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180

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Db 652 ATCTATGCCCTTCTGCTGGGAATTCNCCTCTTTGGCTTCTACTGGCTGGGTGTGTATCAG 711
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPhe 196
Db 712 CTAGGAACATATATTTGGAAAAGGAATTGCCANNAGTGGAGACACATTT 759

RESULT 14
CO249306 854 bp mRNA linear EST 23-JUN-2004
LOCUS AGENCOURT 25900925 NIH MGC 195 Homo sapiens cDNA clone
DEFINITION IMAGE:7286360 5', mRNA_sequence.
ACCESSION CO249306
VERSION CO249306.1 GI:49120079
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 854)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 584.

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      loxP-HindIII; Clones from this library have been
      PCR-amplified using gene-specific primers to contain the
      complete open reading frame (based on known gene sequences
      available from NCBI's RefSeq). Template for PCR is cDNA
      derived from either pooled cytoplasmic polyA RNA from 30
      cells lines or pooled total RNA from 10 different tissues
      (from BD Biosciences/clontech and Washington University).
      PCR products are directionally cloned into the loxP sites
      of the pDNR-Dual vector. Library constructed by Dr.
      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
      Expression Laboratory, Research Technology Program, SAIC
      Frederick, NCI-Frederick, Frederick, MD 21702). For
      information on which gene each clone represents, please
      visit our anonymous ftp site at
      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
      a Note: this is a NIH_MGC Library."

ORIGIN
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Best Local Similarity: 84.82% Mismatches: 17
Query Match: 49.52% Indels: 4
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 832)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg 31 Rm10A07 Bethesda, MD 20892  
 Email: gcgabs-r@mail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 CDNA Library Preparation: Bhat Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
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 Plate: IRBK8 row: 9 column: 09  
 High quality sequence start: 16  
 High quality sequence stop: 628.

FEATURES  
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 loxP-HindIII; Clones from this library have been  
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 visit our anonymous ftp site at  
 ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
 a Note: this is a NIH MGC library."

ORIGIN

Alignment Scores:  
 Pred. No.: 2,91e-103 Length: 832  
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 Best Local Similarity: 79.67% Mismatches: 28  
 Query Match: 49.34% Indels: 6  
 DB: 7 Gaps: 1  
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